

μL of the diluted conjugate was added to each well and incubated for 30 minutes at room temperature. Following incubation, the wells were washed five times with PBS/0.1% Tween 20™. 100 μL of tetramethylbenzidine peroxidase (TMB) substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) was added, undiluted, and  
5 incubated for about 15 minutes. The reaction was stopped with the addition of 100 μL of 1 N H<sub>2</sub>SO<sub>4</sub> to each well, and the plates were read at 450 nm.

Figure 4 shows the ELISA reactivity of two recombinant antigens isolated using method A in Example 3 (TbRa3 and TbRa9) with sera from *M. tuberculosis* positive and negative patients. The reactivity of these antigens is  
10 compared to that of bacterial lysate isolated from *M. tuberculosis* strain H37Ra (Difco, Detroit, MI). In both cases, the recombinant antigens differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 56 out of 87 positive sera, and TbRa9 detected 111 out of 165 positive sera.

Figure 5 illustrates the ELISA reactivity of representative antigens  
15 isolated using method B of Example 3. The reactivity of the recombinant antigens TbH4, TbH12, Tb38-1 and the peptide TbM-1 (as described in Example 4) is compared to that of the 38 kD antigen described by Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989. Again, all of the polypeptides tested differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbH4  
20 detected 67 out of 126 positive sera, TbH12 detected 50 out of 125 positive sera, 38-1 detected 61 out of 101 positive sera and the TbM-1 peptide detected 25 out of 30 positive sera.

The reactivity of four antigens (TbRa3, TbRa9, TbH4 and TbH12) with sera from a group of *M. tuberculosis* infected patients with differing reactivity in the  
25 acid fast stain of sputum (Smithwick and David, *Tubercle* 52:226, 1971) was also examined, and compared to the reactivity of *M. tuberculosis* lysate and the 38 kD antigen. The results are presented in Table 3, below:

TABLE 3

REACTIVITY OF ANTIGENS WITH SERA FROM *M. TUBERCULOSIS* PATIENTS

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-2	++++	1.853	0.634	0.998	1.022	1.030	1.314
Tb01B93I-19	++++	2.657	2.322	0.608	0.837	1.857	2.335
Tb01B93I-8	+++	2.703	0.527	0.492	0.281	0.501	2.002
Tb01B93I-10	+++	1.665	1.301	0.685	0.216	0.448	0.458
Tb01B93I-11	+++	2.817	0.697	0.509	0.301	0.173	2.608
Tb01B93I-15	+++	1.28	0.283	0.808	0.218	1.537	0.811
Tb01B93I-16	+++	2.908	>3	0.899	0.441	0.593	1.080
Tb01B93I-25	+++	0.395	0.131	0.335	0.211	0.107	0.948
Tb01B93I-87	+++	2.653	2.432	2.282	0.977	1.221	0.857
Tb01B93I-89	---	1.912	2.370	2.436	0.876	0.520	0.952
Tb01B94I-108	---	1.639	0.341	0.797	0.368	0.654	0.798
Tb01B94I-201	---	1.721	0.419	0.661	0.137	0.064	0.692
Tb01B93I-88	---	1.939	1.269	2.519	1.381	0.214	0.530
Tb01B93I-92	---	2.355	2.329	2.78	0.685	0.997	2.527
Tb01B94I-109	++	0.993	0.620	0.574	0.441	0.5	2.558
Tb01B94I-210	++	2.777	>3	0.393	0.367	1.004	1.315
Tb01B94I-224	++	2.913	0.476	0.251	1.297	1.990	0.256
Tb01B93I-9	-	2.649	0.278	0.210	0.140	0.181	1.586
Tb01B93I-14	+	>3	1.538	0.282	0.291	0.549	2.880
Tb01B93I-21	-	2.645	0.739	2.499	0.783	0.536	1.770

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-22	+	0.714	0.451	2.082	0.285	0.269	1.159
Tb01B93I-31	+	0.956	0.490	1.019	0.812	0.176	1.293
Tb01B93I-32	-	2.261	0.786	0.668	0.273	0.535	0.405
Tb01B93I-52	-	0.658	0.114	0.434	0.330	0.273	1.140
Tb01B93I-99	-	2.118	0.584	1.62	0.119	0.977	0.729
Tb01B94I-130	-	1.349	0.224	0.86	0.282	0.383	2.146
Tb01B94I-131	-	0.685	0.324	1.173	0.059	0.118	1.431
AT4-0070	Normal	0.072	0.043	0.092	0.071	0.040	0.039
AT4-0105	Normal	0.397	0.121	0.118	0.103	0.078	0.390
3/15/94-1	Normal	0.227	0.064	0.098	0.026	0.001	0.228
4/15/93-2	Normal	0.114	0.240	0.071	0.034	0.041	0.264
5/26/94-4	Normal	0.089	0.259	0.096	0.046	0.008	0.053
5/26/94-3	Normal	0.139	0.093	0.085	0.019	0.067	0.01

Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 23 out of 27 positive sera, TbRa9 detected 22 out of 27, TbH4 detected 18 out of 27 and TbH12 detected 15 out of 27. If used in combination, these four antigens would have a theoretical sensitivity of 27 out of 27, indicating that these antigens should complement each other in the serological detection of *M. tuberculosis* infection. In addition, several of the recombinant antigens detected positive sera that were not detected using the 38 kD antigen, indicating that these antigens may be complementary to the 38 kD antigen.

The reactivity of the recombinant antigen TbRa11 with sera from *M. tuberculosis* patients shown to be negative for the 38 kD antigen, as well as with sera from PPD positive and normal donors, was determined by ELISA as described above.

The results are shown in Figure 6 which indicates that TbRa11, while being negative with sera from PPD positive and normal donors, detected sera that were negative with the 38 kD antigen. Of the thirteen 38 kD negative sera tested, nine were positive with TbRa11, indicating that this antigen may be reacting with a sub-group of 38 kD antigen negative sera. In contrast, in a group of 38 kD positive sera where TbRa11 was reactive, the mean OD 450 for TbRa11 was lower than that for the 38 kD antigen. The data indicate an inverse relationship between the presence of TbRa11 activity and 38 kD positivity.

The antigen TbRa2A was tested in an indirect ELISA using initially 50  $\mu$ l of serum at 1:100 dilution for 30 minutes at room temperature followed by washing in PBS Tween and incubating for 30 minutes with biotinylated Protein A (Zymed, San Francisco, CA) at a 1:10,000 dilution. Following washing, 50  $\mu$ l of streptavidin-horseradish peroxidase (Zymed) at 1:10,000 dilution was added and the mixture incubated for 30 minutes. After washing, the assay was developed with TMB substrate as described above. The reactivity of TbRa2A with sera from *M. tuberculosis* patients and normal donors is shown in Table 4. The mean value for reactivity of TbRa2A with sera from *M. tuberculosis* patients was 0.444 with a standard deviation of 0.309. The mean for reactivity with sera from normal donors was 0.109 with a standard deviation of 0.029. Testing of 38 kD negative sera (Figure 7) also indicated that the TbRa2A antigen was capable of detecting sera in this category.

TABLE 4  
REACTIVITY OF TBRA2A WITH SERA FROM *M. TUBERCULOSIS* PATIENTS AND FROM  
NORMAL DONORS

Serum ID	Status	OD 450
Tb85	TB	0.680
Tb86	TB	0.450
Tb87	TB	0.263
Tb88	TB	0.275
Tb89	TB	0.403
Tb91	TB	0.393
Tb92	TB	0.401

Tb93	TB	0.232
Tb94	TB	0.333
Tb95	TB	0.435
Tb96	TB	0.284
Tb97	TB	0.320
Tb99	TB	0.328
Tb100	TB	0.817
Tb101	TB	0.507
Tb102	TB	0.191
Tb103	TB	0.228
Tb107	TB	0.324
Tb109	TB	1.572
Tb112	TB	0.338
DL4-0176	Normal	0.036
AT4-0043	Normal	0.126
AT4-0044	Normal	0.130
AT4-0052	Normal	0.135
AT4-0053	Normal	0.133
AT4-0062	Normal	0.128
AT4-0070	Normal	0.088
AT4-0091	Normal	0.108
AT4-0100	Normal	0.106
AT4-0105	Normal	0.108
AT4-0109	Normal	0.105

The reactivity of the recombinant antigen (g) (SEQ ID NO: 60) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. Figure 3 shows the results of the titration of antigen (g) with four *M. tuberculosis* positive sera that were all reactive with the 38 kD antigen and with four donor sera. All four positive sera were reactive with antigen (g).

The reactivity of the recombinant antigen TbH-29 (SEQ ID NO: 137) with sera from *M. tuberculosis* patients, PPD positive donors and normal donors was determined by indirect ELISA as described above. The results are shown in Figure 9. TbH-29 detected 30 out of 60 *M. tuberculosis* sera, 2 out of 8 PPD positive sera and 2 out of 27 normal sera.

Figure 10 shows the results of ELISA tests (both direct and indirect) of the antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors and with a pool of sera from *M. tuberculosis* patients. The mean

OD 450 was demonstrated to be higher with sera from *M. tuberculosis* patients than from normal donors, with the mean OD 450 being significantly higher in the indirect ELISA than in the direct ELISA. Figure 11 is a titration curve for the reactivity of recombinant TbH-33 with sera from *M. tuberculosis* patients and from normal donors showing an increase in OD 450 with increasing concentration of antigen.

The reactivity of the recombinant antigens RDIF6, RDIF8 and RDIF10 (SEQ ID NOS: 184-187, respectively) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. RDIF6 detected 6 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; RDIF8 detected 14 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; and RDIF10 detected 4 out of 27 *M. tuberculosis* sera and 1 out of 15 normal sera. In addition, RDIF10 was found to detect 0 out of 5 sera from PPD-positive donors.

The antigens MO-1, MO-2, MO-4, MO-28 and MO-29 described above in Example 5, were expressed in *E. coli* and purified using a hexahistidine tag. The reactivity of these antigens with both *M. tuberculosis* positive and negative sera was examined by ELISA as described above. Titration curves showing the reactivity of MO-1, MO-2, MO-4, MO-28 and MO-29 at different solid phase coat levels when tested against four *M. tuberculosis* positive sera and four *M. tuberculosis* negative sera are shown in Figs. 12A-E, respectively. Three of the clones, MO-1, MO-2 and MO-29 were further tested on panels of HIV positive/tuberculosis (HIV/TB) positive and extrapulmonary sera. MO-1 detected 3/20 extrapulmonary and 2/38 HIV/TB sera. On the same sera groups, MO-2 detected 2/20 and 10/38, and MO-29 detected 2/20 and 8/38 sera. In combination these three clones would have detected 4/20 extrapulmonary sera and 16/38 HIV/TB sera. In addition, MO-1 detected 6/17 sera that had previously been shown only to react with *M. tuberculosis* lysate and not with either 38 kD or with other antigens of the subject invention.

### EXAMPLE 10

#### PREPARATION AND CHARACTERIZATION OF *M. TUBERCULOSIS* FUSION PROTEINS

A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was  
5 prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified  
by PCR in order to facilitate their fusion and the subsequent expression of the fusion  
protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform  
PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 141 and 142), PDM-57 and  
10 PDM-58 (SEQ ID NO: 143 and 144), and PDM-69 and PDM-60 (SEQ ID NO: 145-  
146), respectively. In each case, the DNA amplification was performed using 10  $\mu$ l  
10X Pfu buffer, 2  $\mu$ l 10 mM dNTPs, 2  $\mu$ l each of the PCR primers at 10  $\mu$ M  
concentration, 81.5  $\mu$ l water, 1.5  $\mu$ l Pfu DNA polymerase (Stratagene, La Jolla, CA)  
and 1  $\mu$ l DNA at either 70 ng/ $\mu$ l (for TbRa3) or 50 ng/ $\mu$ l (for 38 kD and Tb38-1). For  
15 TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C  
for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at  
96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15  
sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C  
for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for  
20 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by  
72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned  
directly into pT7<sup>+</sup>L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment  
was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and  
25 then digested with EcoRI for direct cloning into the pT7<sup>+</sup>L2Ra3-1 vector which was  
digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and  
EcoRI and directly subcloned into pT7<sup>+</sup>L2Ra3/38kD-17 digested with the same  
enzymes. The whole fusion was then transferred to pET28b using NdeI and EcoRI  
sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed to BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD<sub>560</sub> of 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 25,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 147 and 148, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 151.

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO: 145 and PDM-83 (SEQ ID NO: 200) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DnaI site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and PDM-85 (SEQ ID NO: 201 and 202, respectively) and 1 µl DNA at 50 ng/µl.



Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 203 and 204, respectively.

10 A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.

Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 343 and 344, respectively) and 2 µl DNA at 100 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min; and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sca I (New England Biolabs.) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 345 and 346, respectively.

A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.

25 38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 347 and 348, respectively), and 1 µl PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec; and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and

then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7AL2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7AL2 construct was designed to have a  
5 MGHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn 2I (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New  
10 England Biolabs) and Eco RI. Ligations were done with a ligation kit from Panvera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared essentially as described above. The  
15 DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 349 and 350, respectively.

## EXAMPLE 11

### USE OF *M. TUBERCULOSIS* FUSION PROTEINS FOR SERODIAGNOSIS OF TUBERCULOSIS

The effectiveness of the fusion protein TbRa3-38 kD-Tb38-1, prepared  
as described above, in the serodiagnosis of tuberculosis infection was examined by  
25 ELISA.

The ELISA protocol was as described above in Example 6, with the  
fusion protein being coated at 200 ng/well. A panel of sera was chosen from a group of  
tuberculosis patients previously shown, either by ELISA or by western blot analysis, to  
react with each of the three antigens individually or in combination. Such a panel  
30 enabled the dissection of the serological reactivity of the fusion protein to determine if

all three epitopes functioned with the fusion protein. As shown in Table 5, all four sera that reacted with TbRa3 only were detectable with the fusion protein. Three sera that reacted only with Tb38-1 were also detectable, as were two sera that reacted with 38 kD alone. The remaining 15 sera were all positive with the fusion protein based on a cut-off in the assay of mean negatives +3 standard deviations. This data demonstrates the functional activity of all three epitopes in the fusion protein.

TABLE 5  
REACTIVITY OF TRI-PEPTIDE FUSION PROTEIN WITH SERA FROM *M. TUBERCULOSIS* PATIENTS

Serum ID	Status	ELISA and/or Western Blot Reactivity with Individual proteins			Fusion Recombinant OD 450	Fusion Recombinant Status
		38kd	Tb38-1	TbRa3		
01B93I-40	TB	-	-	+	0.413	+
01B93I-41	TB	-	+	+	0.392	+
01B93I-29	TB	+	-	+	2.217	+
01B93I-109	TB	+	±	+	0.522	+
01B93I-132	TB	±	+	-	0.937	+
5004	TB	±	-	±	1.098	+
15004	TB	+	+	-	2.077	+
39004	TB	+	±	-	1.675	+
68004	TB	+	±	±	2.388	+
99004	TB	-	+	±	0.607	+
107004	TB	-	+	±	0.667	+
92004	TB	±	±	±	1.070	+
97004	TB	+	-	±	1.152	+
118004	TB	+	-	±	2.694	+
173004	TB	+	+	+	3.258	+
175004	TB	+	-	+	2.514	+
274004	TB	-	-	+	3.220	+
276004	TB	-	+	-	2.991	+
282004	TB	+	-	-	0.824	+
289004	TB	-	-	+	0.848	+

308004	TB	-	+	-	3.338	+
314004	TB	-	+	-	1.362	+
317004	TB	+	-	-	0.763	+
312004	TB	-	-	+	1.079	+
D176	PPD	-	-	-	0.145	-
D162	PPD	-	-	-	0.073	-
D161	PPD	-	-	-	0.097	-
D27	PPD	-	-	-	0.082	-
A6-124	NORMAL	-	-	-	0.053	-
A6-125	NORMAL	-	-	-	0.087	-
A6-126	NORMAL	-	-	-	0.346	-
A6-127	NORMAL	-	-	-	0.064	-
A6-128	NORMAL	-	-	-	0.034	-
A6-129	NORMAL	-	-	-	0.037	-
A6-130	NORMAL	-	-	-	0.057	-
A6-131	NORMAL	-	-	-	0.054	-
A6-132	NORMAL	-	-	-	0.022	-
A6-133	NORMAL	-	-	-	0.147	-
A6-134	NORMAL	-	-	-	0.101	-
A6-135	NORMAL	-	-	-	0.066	-
A6-136	NORMAL	-	-	-	0.054	-
A6-137	NORMAL	-	-	-	0.065	-
A6-138	NORMAL	-	-	-	0.041	-
A6-139	NORMAL	-	-	-	0.103	-
A6-140	NORMAL	-	-	-	0.212	-
A6-141	NORMAL	-	-	-	0.056	-
A6-142	NORMAL	-	-	-	0.051	-

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 6) demonstrate that all four antigens function independently in the fusion protein.

TABLE 6

REACTIVITY OF TbF-2 FUSION PROTEIN WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa3	Tb38-1	DPEP
B931-40	TB	0.57	+	0.321	+	-	-	-	-
B931-41	TB	0.601	+	0.396	+	-	-	-	-
B931-109	TB	0.494	+	0.404	+	+	+	+	-
B931-132	TB	1.502	+	1.292	+	+	+	+	-
5004	TB	1.806	+	1.666	+	+	+	+	+
15004	TB	2.862	+	2.468	+	+	+	+	-
38004	TB	2.443	+	1.722	+	+	+	+	-
68004	TB	2.871	+	2.375	+	+	+	+	-
98004	TB	0.691	-	0.971	-	-	-	-	-
107004	TB	0.875	-	0.732	-	-	-	-	-
92004	TB	1.632	-	1.394	-	-	-	-	-
97004	TB	1.491	-	1.979	-	-	-	-	-
118004	TB	3.182	+	3.045	+	+	+	+	+
173004	TB	3.644	+	3.578	+	+	+	+	-
175004	TB	3.332	+	2.916	+	+	+	+	-
274004	TB	3.696	+	3.716	+	+	+	+	-
276004	TB	3.243	+	2.56	+	+	+	+	-
282004	TB	1.249	-	1.234	-	-	-	-	-
289004	TB	1.375	-	1.17	-	-	-	-	-
308004	TB	3.708	+	3.353	+	+	+	+	-
314004	TB	1.663	-	1.399	-	-	-	-	-
317004	TB	1.163	-	0.92	-	-	-	-	-
312004	TB	1.789	-	1.453	-	-	-	-	-
380004	TB	0.238	-	0.461	-	-	-	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
478004	TB	0.188	-	0.469	-	-	-	-	-
419004	TB	0.384	-	2.392	-	+	+	+	+
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.357	-	1.456	-	-	-	-	-
328004	TB	0.047	-	0.196	-	-	-	-	-
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.123	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.133	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.123	-	0.12	-	-	-	-	-
Cut-off		0.284		0.266					

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the  
5 construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the  
10 invention.

## CLAIMS

We claim:

1. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 117);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 119);
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123); and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132), wherein Xaa may be any amino acid.

3. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.



6. A recombinant expression vector comprising a DNA molecule according to claim 5.
7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
  - (a) contacting a biological sample with one or more polypeptides according to any of claims 1-4; and
  - (b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.
10. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
  - (a) contacting a biological sample with a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
  - (b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.
11. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
  - (a) contacting a biological sample with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said

sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

12. The method of any one of claims 9-11 wherein step (a) additionally comprises contacting the biological sample with a 38 kD *M. tuberculosis* antigen and step (b) additionally comprises detecting in the sample the presence of antibodies that bind to the 38 kD *M. tuberculosis* antigen.

13. The method of any one of claims 9-11 wherein the polypeptide(s) are bound to a solid support.

14. The method of claim 13 wherein the solid support comprises nitrocellulose, latex or a plastic material.

15. The method of any one of claims 9-11 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

16. The method of claim 15 wherein the biological sample is whole blood or serum.

17. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

18. The method of claim 17, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 5.

19. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

20. The method of claim 19, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

21. The method of claims 17 or 19 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

22. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

23. The method of claim 22 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

25. The method of claim 24 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

26. The method of claims 22 or 24 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

27. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1-4; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

28. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

29. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

30. The method of any one of claims 27-29 wherein the binding agent is a monoclonal antibody.

31. The method of any one of claims 27-29 wherein the binding agent is a polyclonal antibody.
32. A diagnostic kit comprising:
- (a) one or more polypeptides according to any of claims 1-4; and
  - (b) a detection reagent.
33. A diagnostic kit comprising:
- (a) one or more polypeptides having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
  - (b) a detection reagent.
34. A diagnostic kit comprising:
- (a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and
  - (b) a detection reagent.
35. The kit of any one of claims 32-34 wherein the polypeptide(s) are immobilized on a solid support.
36. The kit of claim 35 wherein the solid support comprises nitrocellulose, latex or a plastic material.
37. The kit of any one of claims 32-34 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

38. The kit of claim 37 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.
39. The kit of claim 37 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin, dye particles and colloidal particles.
40. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 5.
41. A diagnostic kit according to claim 40, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 5.
42. A diagnostic kit comprising a at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.
43. A diagnostic kit according to claim 42, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.
44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 5.

45. A kit according to claim 44, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

46. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

47. A kit according to claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

48. A monoclonal antibody that binds to a polypeptide according to any of claims 1-4.

49. A polyclonal antibody that binds to a polypeptide according to any of claims 1-4.

50. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

51. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6 (SEQ ID NO: 99).

52. A fusion protein comprising a polypeptide having an N-terminal sequence selected from the group of sequences provided in SEQ ID NOS: 129 and 130.

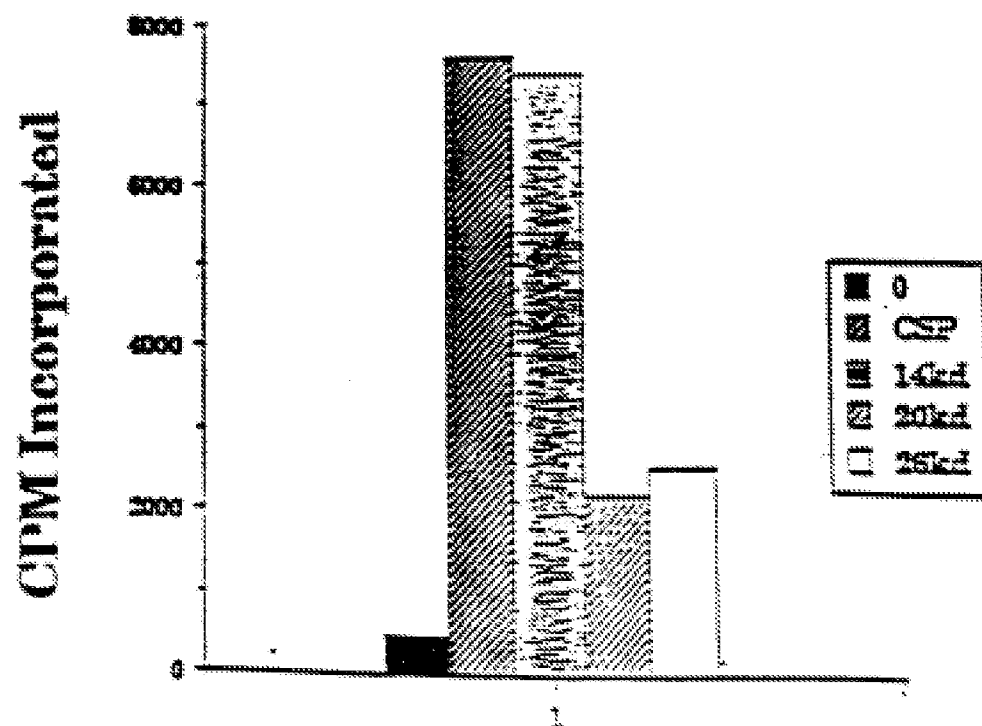


53. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO: 150).

54. A diagnostic kit comprising:

- (a) one or more fusion proteins according to any one of claims 50-53; and
- (b) a detection reagent.

# D7 T Cell Proliferation



## D7 IFN $\gamma$

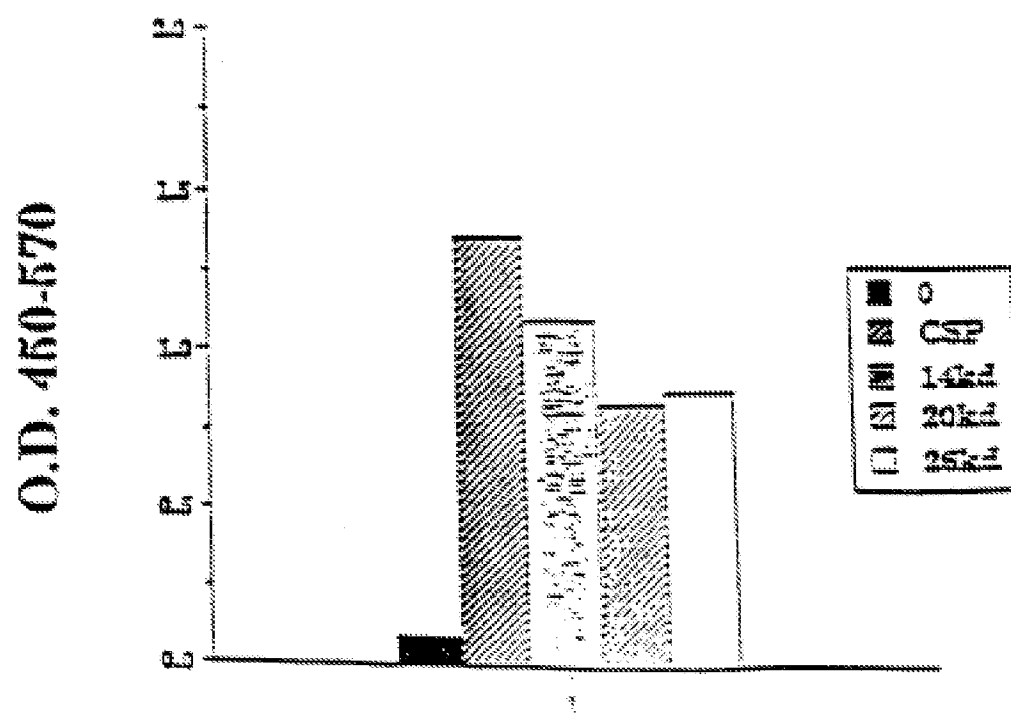
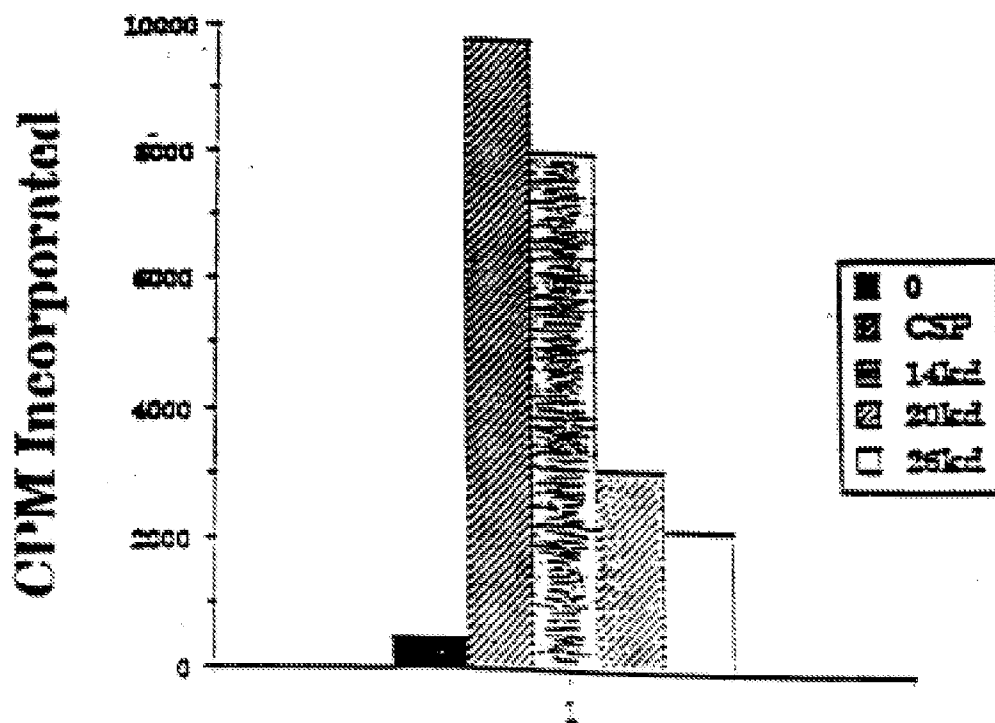


FIG. 1A

## D160 T Cell Proliferation



## D160 IFN $\gamma$

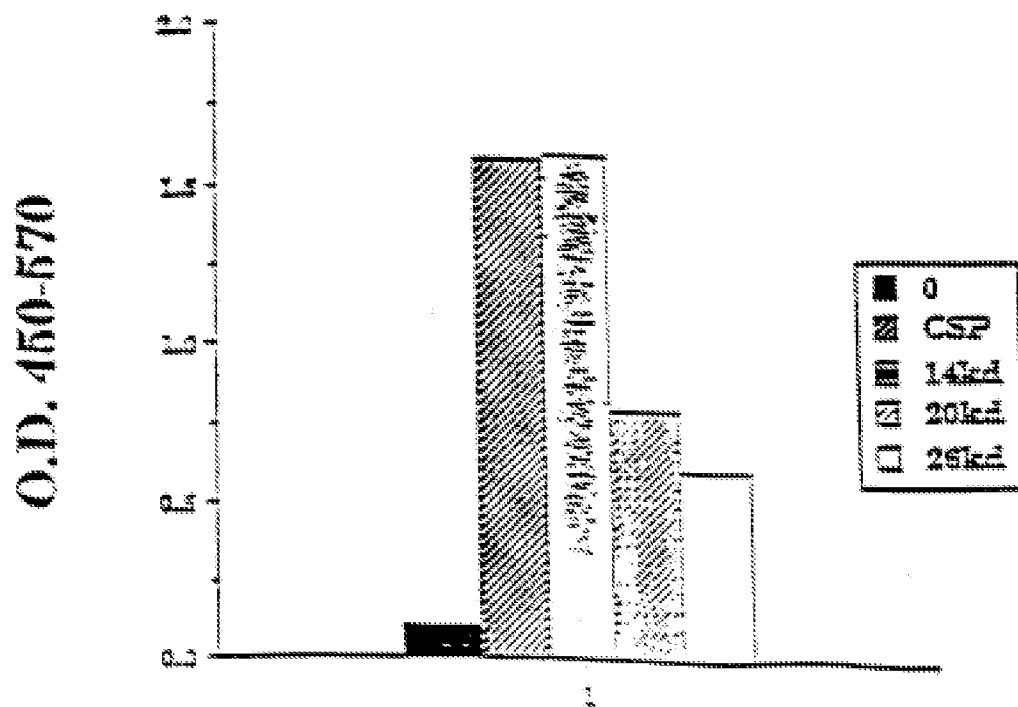
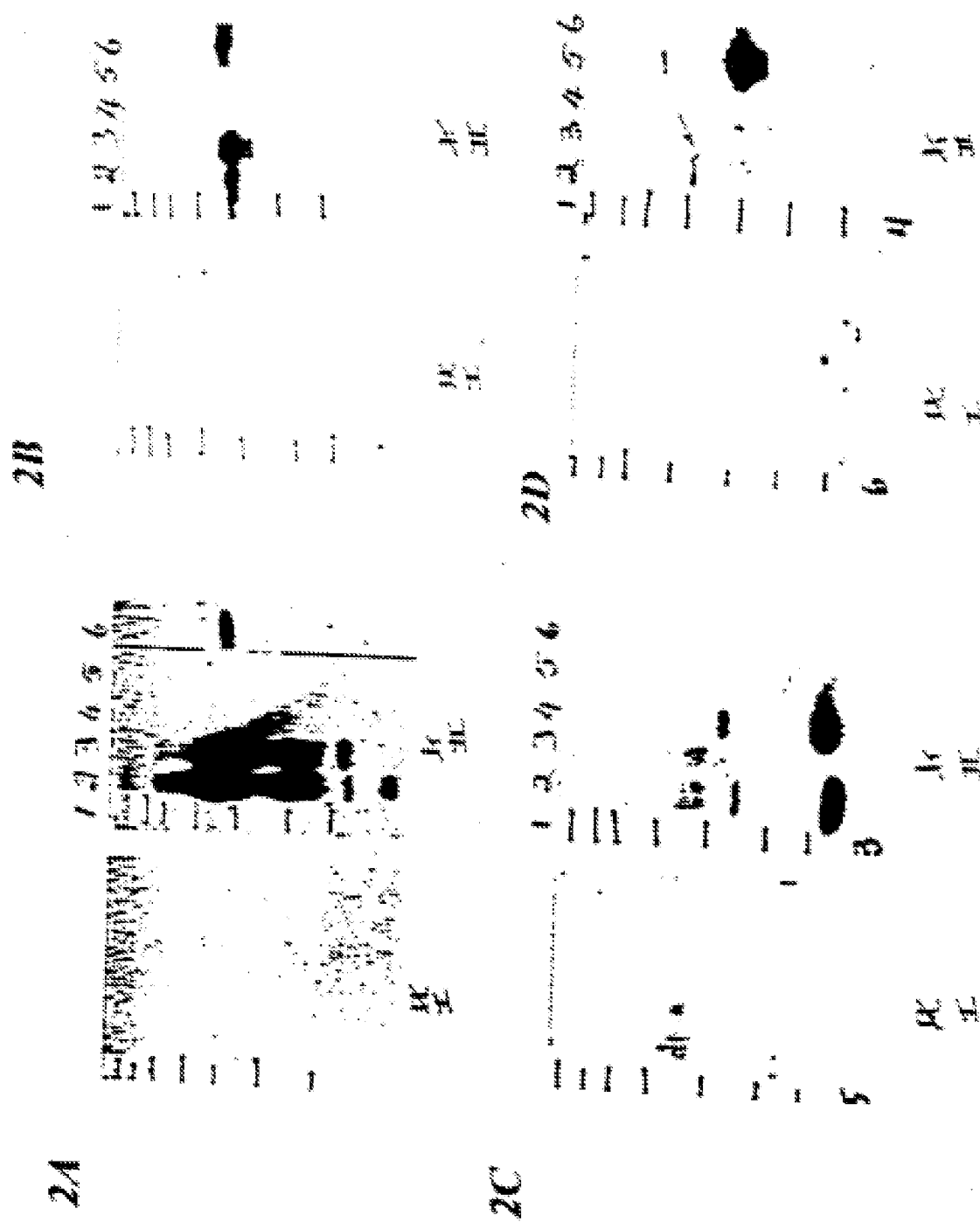


FIG. 1B



FIGS. 2A-D

# T cell clone 131TbH9 responds poorly to CSP

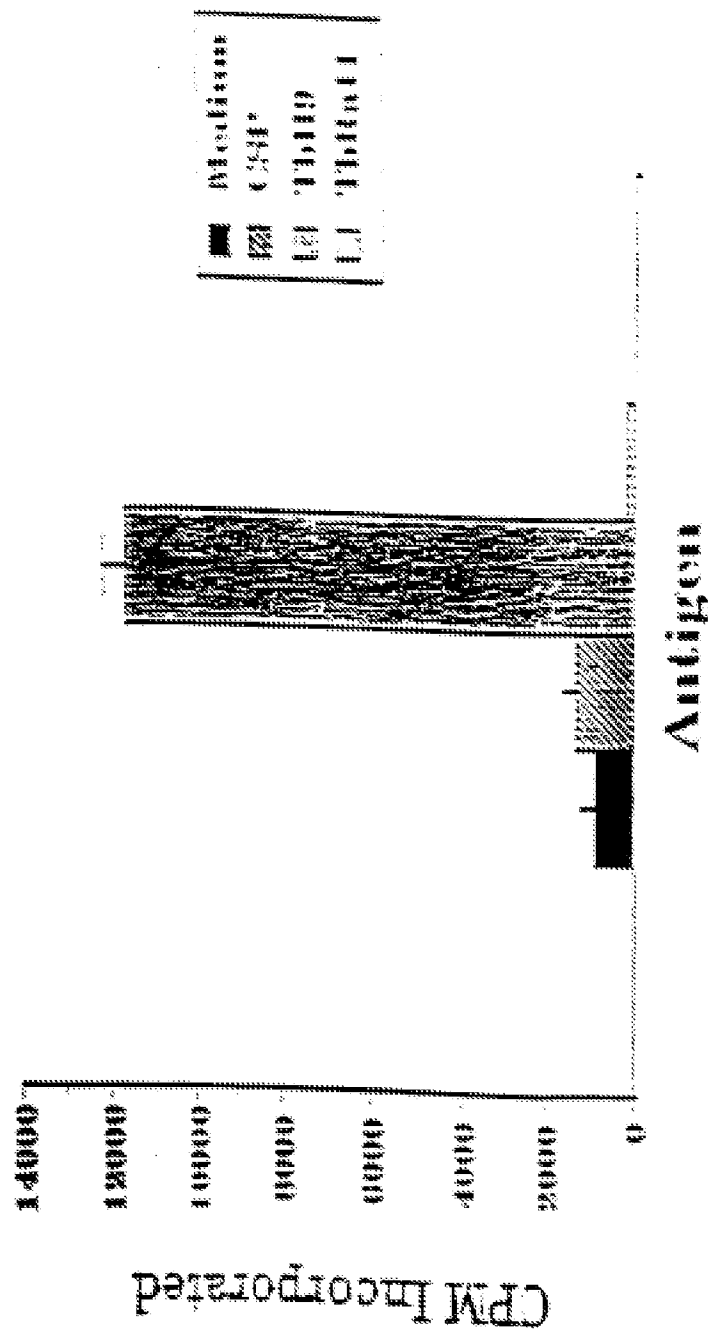


FIG. 3A

# T Cell Clone PPD 800-10 IFN $\gamma$ Production

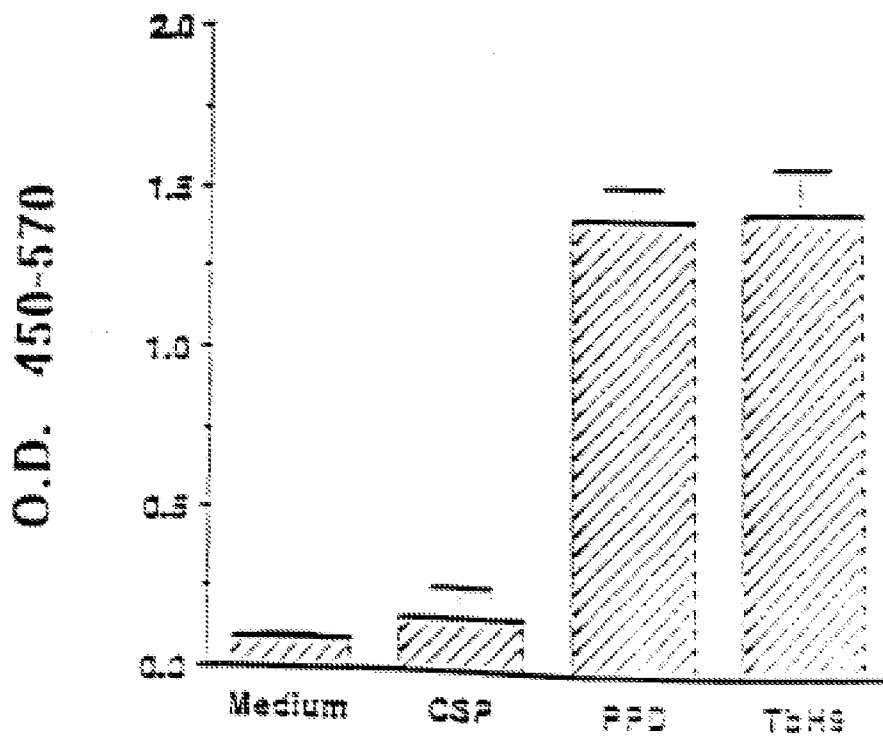


FIG. 3B

FIG. 4

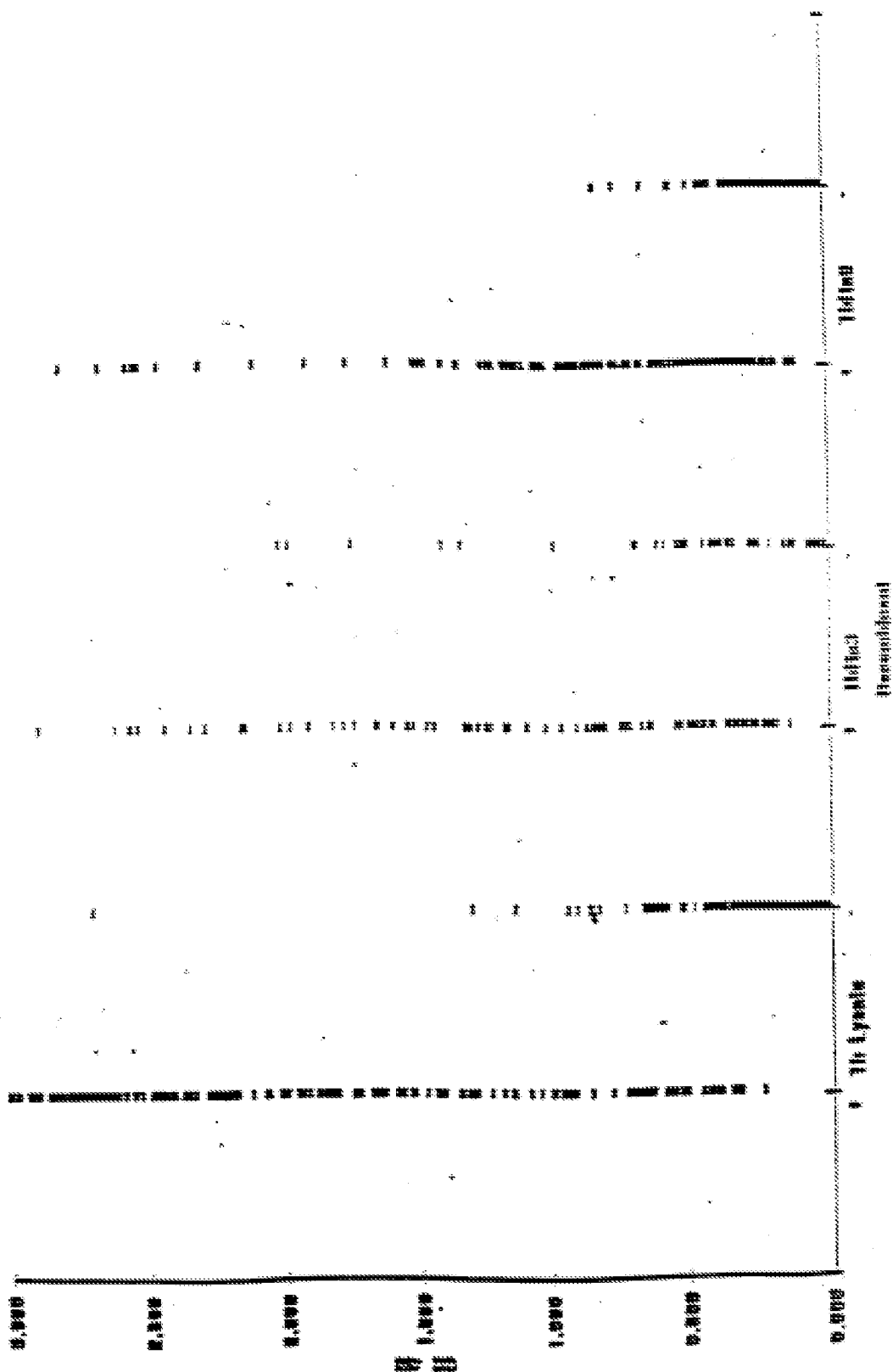


FIG. 4

100

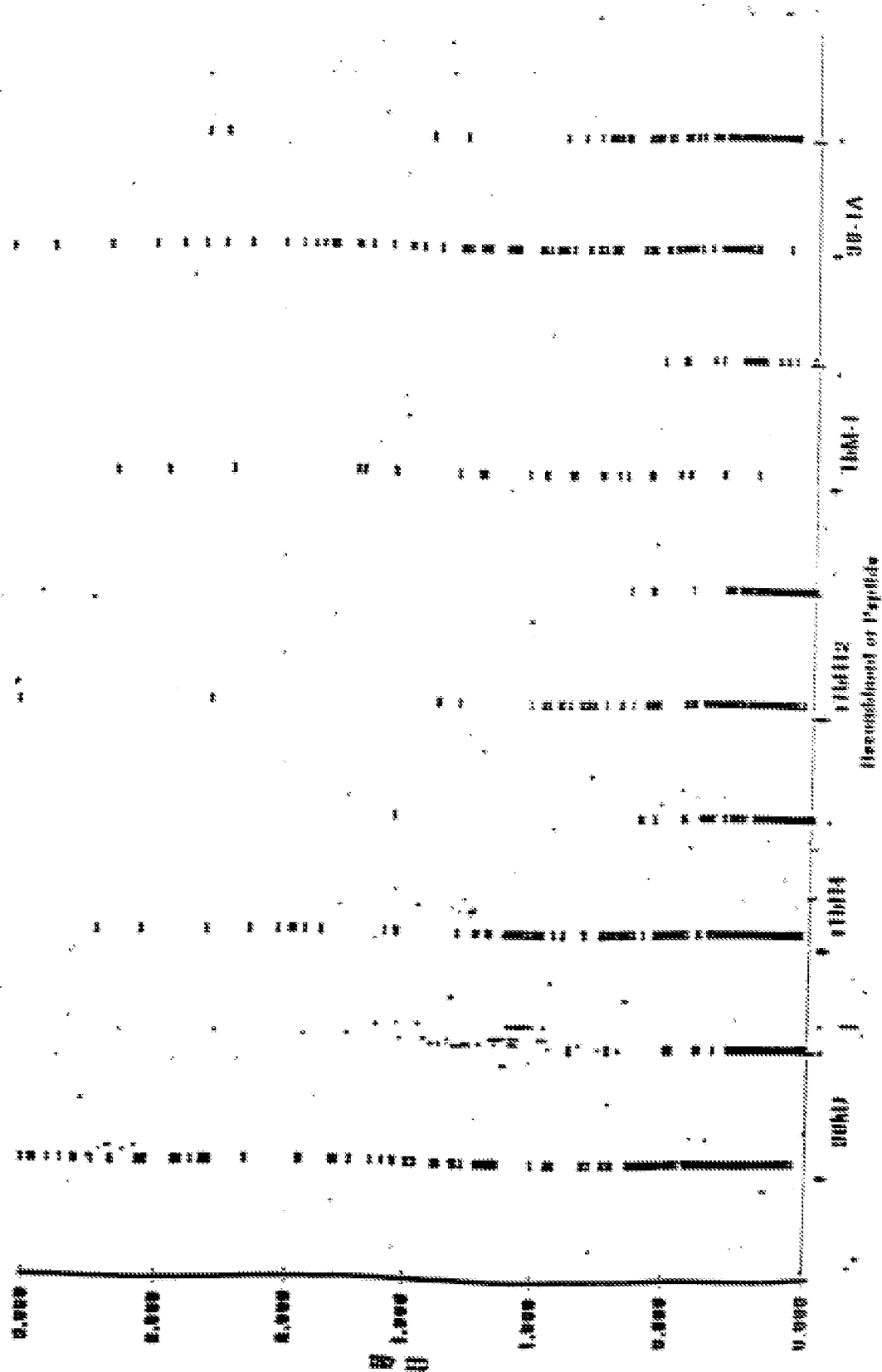
[illegible]



FIG. 6

Identity of Hemophilus (Hsd) and T841 antigen with sera from *M. tuberculosis* patients, PPD positive and normal donors

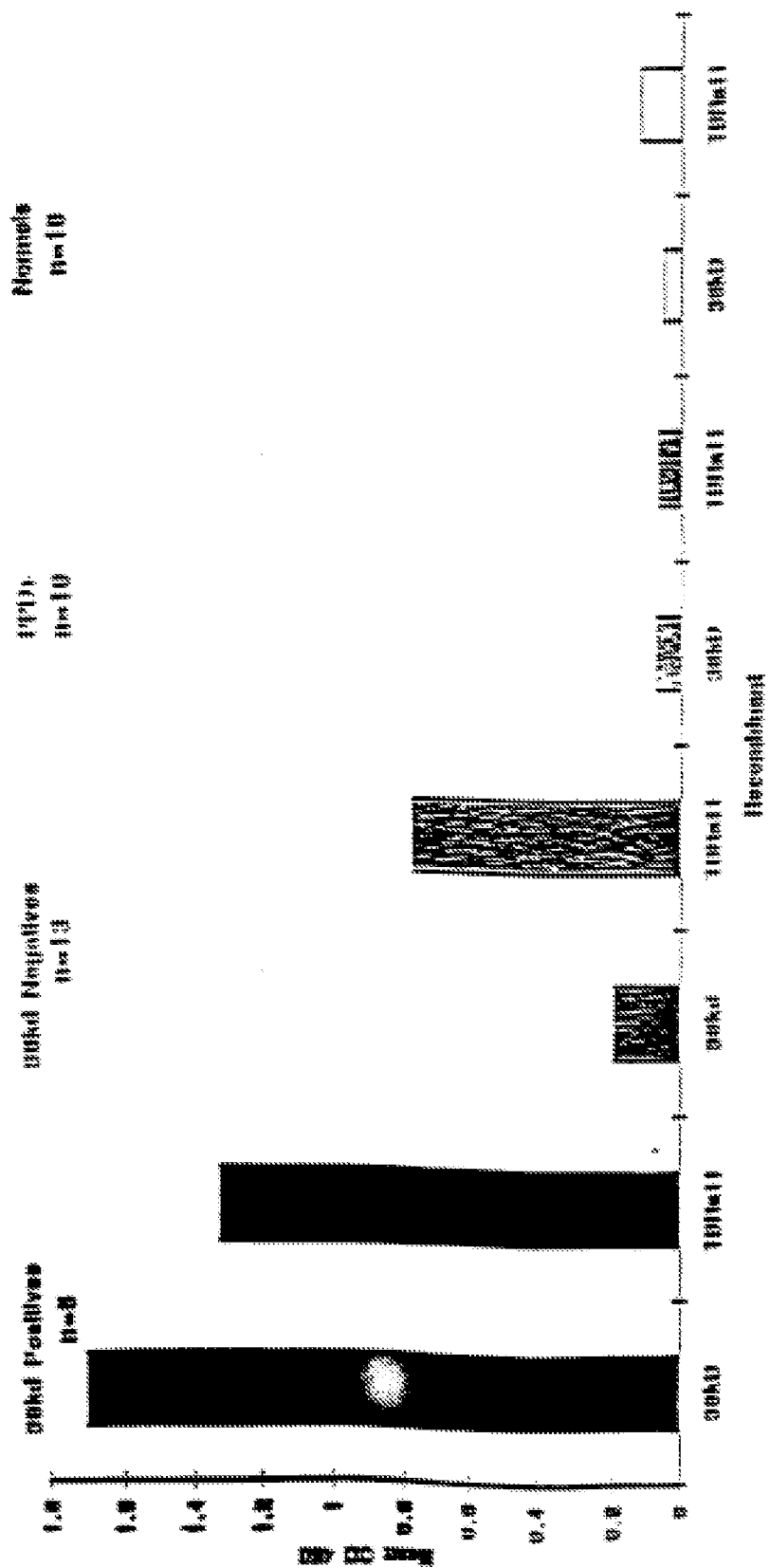
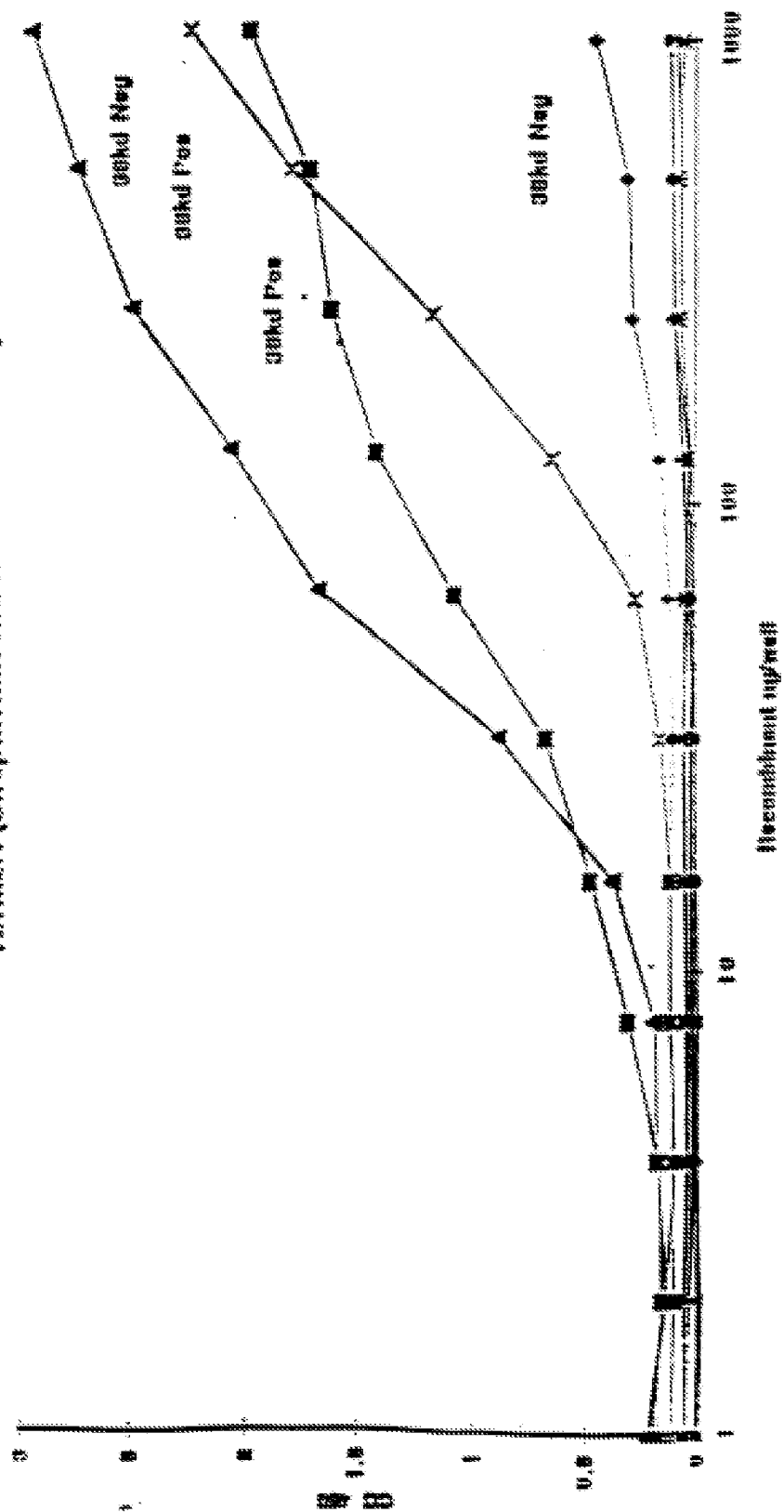


FIG. 7

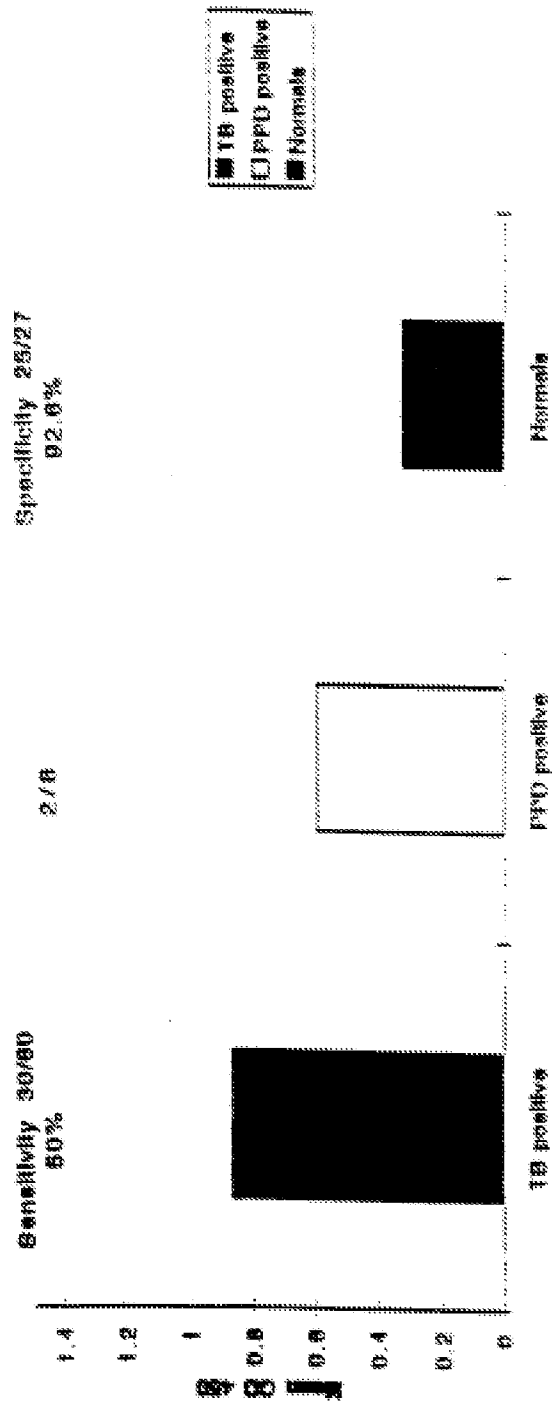
TH1a2A (Sheep/ovine 1007/Protein A Blot)

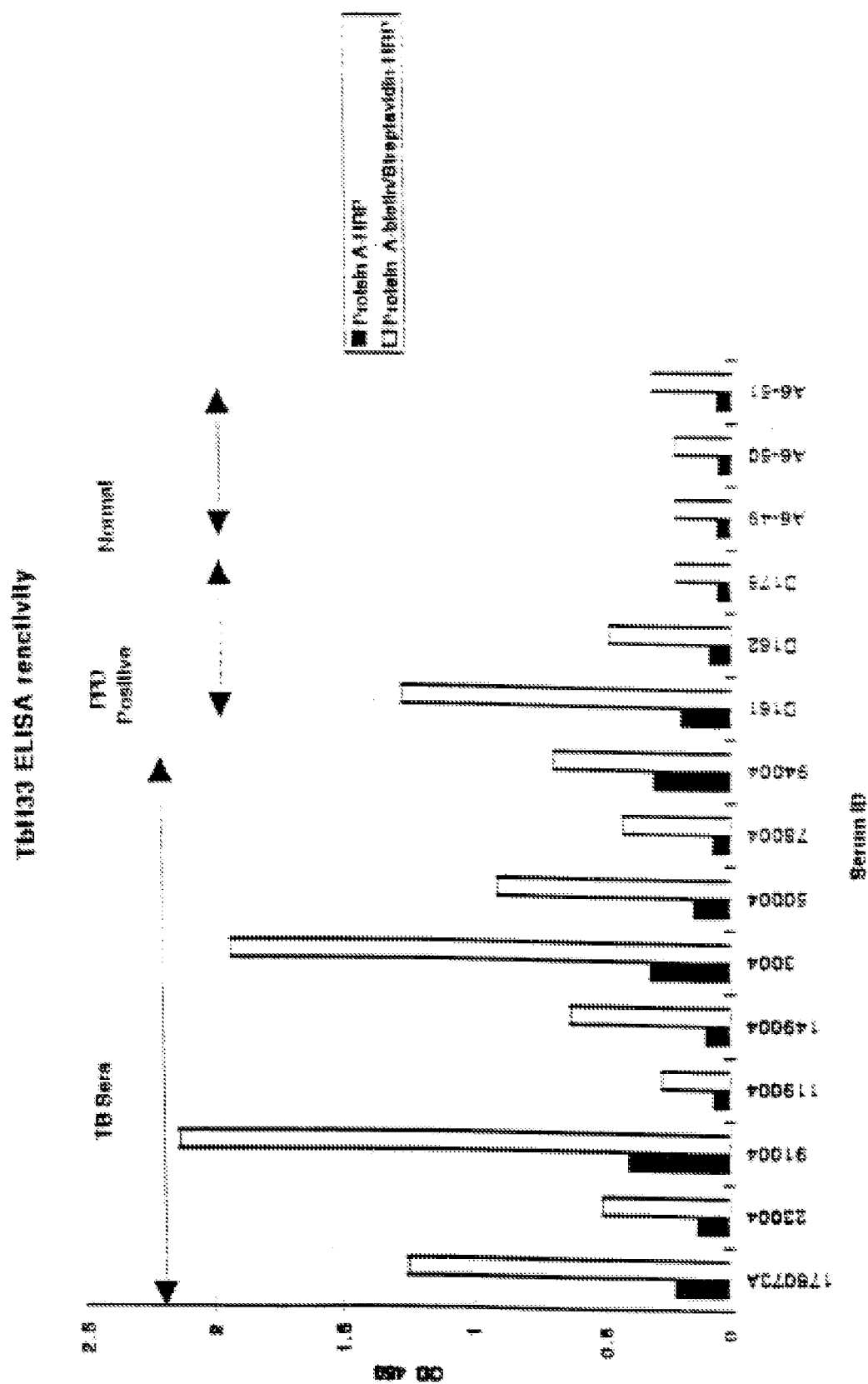




**FIG. 9**

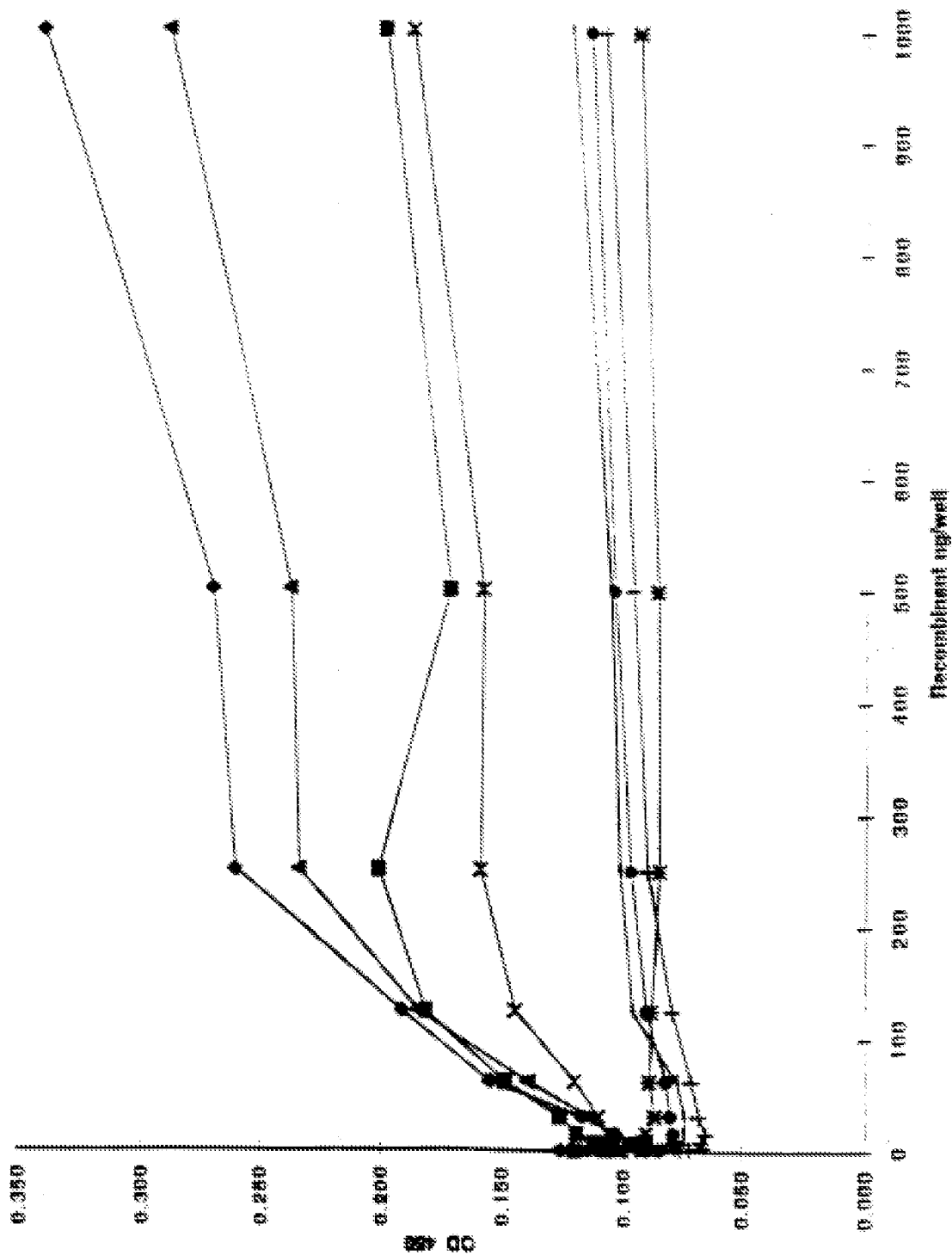
**TbH20 ELISA reactivity in Streptavidin-111P/Protein A-biotin system**



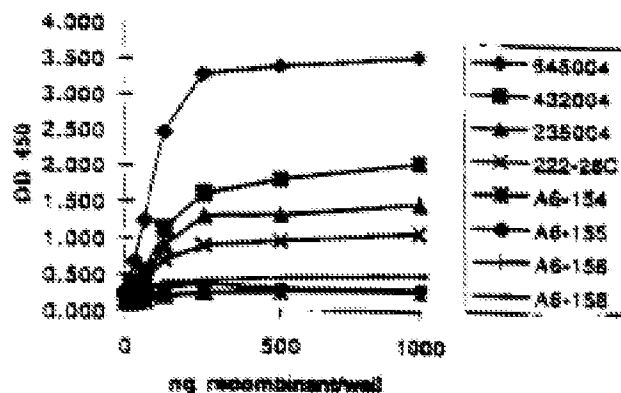


**FIG. 10**

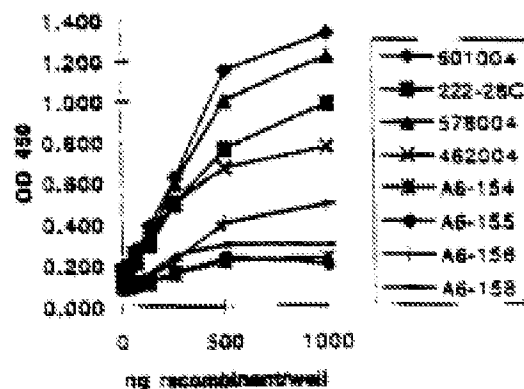
# ELISA reactivity of 1bH33



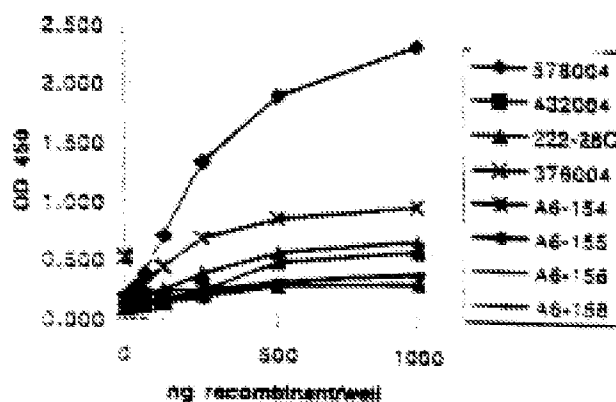
**Titration of Mo-1 antigen with TB positive and negative sera**



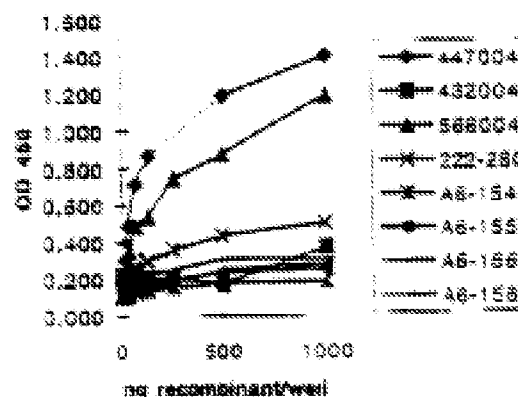
**Titration of Mo-2 with TB positive and negative sera**



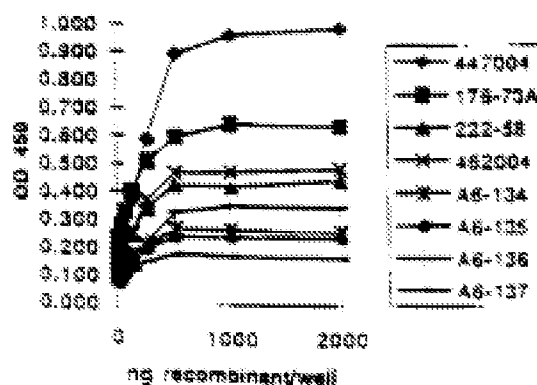
**Titration of Mo-4 with TB positive and negative sera**



**Titration of Mo-28 with TB positive and negative sera**



**Titration of Mo-29 with TB positive and negative sera**



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Reed, Steven G.  
Skeiky, Yasir A.W.  
Dillon, Davin C.  
Campos-Neto, Antonio  
Noughton, Raymond  
Vedvick, Thomas S.  
Twardsik, Daniel R.  
Lodes, Michael J.  
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 350

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104-7092

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 03-MAY-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210221.417C9

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG GTAGTTTGA	CCAAACGCAC AATCGACGG	CAAACCAACG GAAGAACACA	40
ACCATGAAGA TGGTGAATC	GATCGCCSCA GGTCTGACCG	CCGCGGCTGC AATCGGCGCC	120
GCTCGCGGCG GTGTGACTTC	GATCATGGGT GCGCGCCCGG	TGGTATACCA GATCGACGCC	180
GTCTCTCTCG GCGCGGCACT	GCGTTGGAC CCGGCATCG	CCCCGACGT CCGGACCGCC	240
GCCCACTTGA CCAGCTGCT	CAACAGCTTC GCGGATCCCA	ACGTGTCTTT TCGGAACAAG	300
GCGACTCTCG TCGAGGCGCG	CATCGGGGCG ACCGAGGCGC	GCATCGCCCA CCACAAGCTG	360
AAGAAAGCGCG CCGAGCAGCG	GGATCTGCGG CTGTCTTTCA	GCCTGACGAA CATCCAGCCG	420
GCGCGCGCGCG GTTCGGCCAC	CGCCGACGTT TCGCTCTCGG	GTCCGAAGCT CTCTCTCGCG	480
GTCAAGCAGA ACGTCAAGTT	CGTGAATCAA GCGCGGTGGA	TGCTGTCAAG CGCATCGGCG	540
ATGGAACTTC TCGAGGCGCG	AGGNAACTG ATTGGCGGCG	CGGTTTCAGC CCGCTTTTCA	600
GCTACGCGCG CCGCTCTGTC	ACGCTTCAT GTCGAAGACT	CGCGCTGTA GCACGGTGGC	660
GTNTGCGCAG GCGCGCAGCG	ACGCGCGGT GCAAGCGGTC	CTCGAGATAG GTGGTGTCTC	720
GNCACCAAGG ANCAACCCCN	NNTCGNCTNT TCTGCTGNT	GNATGA	766

(2) INFORMATION FOR SEQ ID NO:2:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCAGC ATCACCATCA	CGATCAATTC ACGGTAGAGA	CGACCTCCGT CTTCGCGCGA	60
GACTTCTTCA CCGAGCTGGA	CGCTCTCTCG CAAGCGGGTA	CGGAGAGCGC GGTCTCCGCG	120
GTGGAAAGGC TCCGCGCGCG	CTCGGCGTTG CTGGTACTCA	AACGAGGCCC CAACGCCCGG	180
TCCCGGTTCC TACTCGACCA	AGGCATCAGG TCGGCTGGTC	GGCATCCGUA CAGCGACATA	240
TTTCTCGACG ACGTGACCGT	GAGCGGTGCG CATGCTGAAT	TCCGCTTUGA AAACAACGAA	300
TTCAATGTGG TCGATGTGCG	GAGTGTCAAC GGCACCTAGC	TCAACCGCGA GCGGCTGGAT	360
TGGCGGCTGC TGGCGAACCG	CGACGAGGTC CAGATCGGCA	AGCTCCGGTT GGTGTTCTTG	420
ACCGGACCCA AGCAAGGCGA	GGATGACGCG AGTACCGGCG	GCGGCTGAGC GCACCGGATA	480

GGCCCCGGCT	GGCCCCGATG	TCGATCGGGG	CGGTCTCCG	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTCCAT	TCCTGGGAGG	CTTGAGGGTC	NGGGTGACCC	600
CCCCGGGGGG	CTCATTCCGG	GGTNTGCGCN	GGTTTCACCC	CNTACGACT	GCNCCCGGN	660
TTGCNAATTC	NTTCTTCNCT	GGCCNNAAG	GGACNTTAN	CTTGCCGCTN	GAAAGGTNA	720
TCNCGGGCCC	NTCCTNGAAN	CCGCTTCCCC	CT			752

## (2) INFORMATION FOR SEQ ID NO:3:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCY	AAGGCCCCAG	CGGTGCGGG	GGTTCAGCA	60
CCACGCGACA	CGGGCCCCGA	TCGATCTGCT	AGCTTGAGTC	TGCTCAGGCA	TGCTGCTCAG	120
CAGGCGGATG	GGTATGTTT	GTGCTCGACT	CAGATATCGC	GGGAATCCAA	TCTGCGGCTT	180
GGGGCCCCGG	GTGCTGCAAA	CTACTCCCGG	AGGAATTTCC	ACGTGCGCAT	CAAGATCTTC	240
ATGCTGCTCA	CGGCTGTGCT	TTTCTCTGCT	TGTTGCGGTG	TGGCCACGCG	CGGCCCCGAG	300
ACCTACTGCG	AGGAGTTGAA	AGGCACTCAT	ACGGGCGAGG	CGTGCCAGAT	TCAAATGTCC	360
GACCGGCGCT	ACAACATCAA	CATCAGGCTG	CCGATTACT	ACCGGACCA	GAAGTCTCTG	420
GAAAATTACA	TGGCCGAGAC	GGCGGACAAG	TTCTTCAGCG	CGGCCACATC	GTCCACTCCA	480
CGCGAAGCCC	CTTACGAATT	GAATATCACT	TGGCCACAT	ACCAATCCGC	GATACCGCCG	540
CGTGTACGCG	AGGCGGTGCT	GCTCAGGCTC	TACCACAAAG	CGGCGGGCAC	GCACCCAAAG	600
ACCACTTACA	AGGCTTTGGA	TTGGGACCAAG	GCCTATCCCA	AGCCAATCAC	CTATGACACG	660
CTGTGGCAGG	CTGACACCGA	TGCGCTGCCA	GTCTCTTTCC	CCATTGTTGC	AAGGTGAACT	720
GAGCAACGCA	GACCGGAGCA	ACNGGTATCG	ATAGCCCCCN	AATGCCGCGT	TGGAACCCNG	780
TGAAATTATC	ACAACTTCCG	ACTCACNAAA	NAA			813

## (2) INFORMATION FOR SEQ ID NO:4:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATTAAC ACGGCCCGCT CCGATAACTT CCAGCTGTTC CAGGCTGGGC AGGATTCGC	60
CATTCCGATC GGGCAGGCGA TGGCGATCCG GGGCCAGATC CGATCGGCTG GGGGCTCACC	120
CACCGTTTAT ATCGGGGCTA CCGCTTTCCT CCGCTTGGGT GTTGTGACA ACAACGGCAA	180
CGGCGCAGCA GTCCAAGCGG TGTTCGGAG CCGTCCGCGG GCAAGTCTCG GCATCTCCAC	240
CGGCGAGCTG ATCAGCGCGG TCGACGGCGC TCGATCAAC TCGGCGACCG CGATGCGCA	300
CGCGCTTAAC GGGCATCATC CCGGTACCT CATCTCGGTG AACTGGCAA CCAAGTGGG	360
CGGCACGCT ACAGGGAGG TGACATTGGC CGAGGGACCC CCGGCTGAT TTCGTCTGG	420
ATACCACTCG CCGGCGGCGC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GTTCCCGGAG TATCTCGCCC AGCAATGTC TGGCAGCCGC CCAACCGAAT	60
CCGCTGATCC GACTTGGCAG GTTGTGAAAC CCGCCGCGC GCAAGTATCG GTCCATCCCT	120
AGCCCGGCGA CCGCGAGCGC CCGAATGGCG CGATTGAGGA GCGGGGCAAT TTGGCGGGGC	180
CCGCGACCGG CGAGTCCCGG AATGCGCGCA GTGAGGAGGT GGCAGTCAT GCGCAGCTG	240
ATCCAATCAA CCTGATTCG GCTGCGCGG CATTTCACA ATCGAGTAG TGAGCGCAA	300
TGAATGATCG AAAACGGGNG GCGAGCTCCG GTGTCTGGT GGTGNTAGGT GNTGNTCTG	360
GTGNTGNT ATCAGGATST TCTTCGCGA AAGTGTATG CGAGGAACAG GGTGTGCGG	420
NNNNCCNAN GGGTCCNAN CCGNNNTCC TCGCGANAT CANANAGMCG NTTGATGGA	480
NAAAAGGCTG GAGCAGNNNN AANTGNGGN CCAANAANC NNNNNNGNG NNAAGTNGNT	540
NNNTNTTNC ANNNNNNTG NNGNNGNNG NNNCAANGN NNNNNNGNA NNGGNTNTT	600
NAAT	604

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

TTCCANGTCC AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CCGTGGCGGC      60
CGCTCTAGAA CTAGTGKATM YTYNGGCTG CAGGAATYCG GYACGAGCAT TAGGACAGTC      120
TAACGGTCTT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA      180
CGGGTCCGAA CCGTCACCTT CAACCGGCGC CAGTCCCGYA AGCGGCTTTC GCGGGCGCTA      240
CGGATCGGT TTYTCGSSY GTTGGYCGAC GCGGAGGYCG AGGACGACAT CGACCTCGTC      300
ATCTTCACCG GYCGCGATCC GGTGTTCTTC GCGGACTCG ACCTCAAGGT AGCTGGCGCG      360
GCAGACCGCG CTGCGGACA TCTCACCAGG GTGGGCGGCT ATGACCAAGC CCGTGATCGG      420
CGCGATCAAC GCGCGCGCGG TCACCGCGCG GTCGGAATC GCGCTGTACT GCGACATCTT      480
GATCGGCTTC GAGCAGCGCG GTTCGCGCA CACCGACGCG CCGGTGCGGC TGCTGCCAC      540
CTGGGGACTC AGTGTGTGCT TGCGCAAAA GTTCGCGATC GCGTGGCGCG GGTGGATGAG      600
CGTGACCGCG GACTACTGT CCGTGACGCA CGC                                     613

```

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

CGACGACGAC GCGCGCGGAG AGCGGCGCGG AACGGCGATC GACCGCGCGC TGCGGAGAGT      60
CGGCACGACC CAGGAGGAG TCGAATCATG AAATTGTCTA ACCATATTGA GCGGCTCGCG      120
CGCGCGCGAG CCGCGCGCGC GTTCGCGGAG GTCTATGCGG AGCGCGCGCG CGAGTTGCGC      180
CGGCTGCGCG AGCGGCTCGC CATCTGTCTC CCGGAGGAGG GACTGCTCAC CGCGGCTCG      240
CGGACGTTTC GCGAGACACT GTGCTGCGG CAGGTGCGCG GTGCGCGCAA GGAAGCGGTC      300
GCGCGCGCGG TGCGCGGAG CCGCGGCTGC CCGTGGTGGG TCGAGCGACA CACCGCATG      360
CTGTACCGCG CAGGCGAAAC CGACACGCGG GCGCGCATCT TGCGCGGAC AGCAGCTGCG      420
CGCGGTGACG CGAAGCGCGG GTATGTGGCG TGCGCGGAG GAACCGCGAC ACCGCGCGCA      480

```

CGCGCCGGCAC CGTTCCGCCG GGATGTGGCG GCCGAATACC TGGGCACCGC GTTGCAATTC	540
CAC TTCATCG CACGCTGGT CCTGCTGCTG CTGGACGAAA CCTTCCTGCC GGGGGGCCCC	600
CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGA CTGGTGT TCGCCCGCAA GTTCGCGCGC	660
GAGCATCGGC CGGCGCGCTC CACCGCGCGG CTGGAGCGCG GAACGCTGCC CGACGATCTG	720
GCATGGSCAA CACGTCGGA GCCGATAGCA ACCGCGTTCG CGGCGCTGAG CCACCGACTG	780
GACACCGCGC CGCAGCTGCC GGCACCGACT CTTGAGGTGG TCAGGCGGGT CTTGGGGTGG	840
TGGCAGCGCG AGCCAATGCC GATGAGCACT CCTGAGCGA ACGACGACAC CGCCGAGCTG	900
CGGCGCGACT TGCAGCGCG CACCGCTCTT GCGCTGCTGA CCGCGCTGCC CCGCGATCAG	960
GTGACCGAGC AGGAGCTGC CGCGCGCGGA TCGCTGCTCG ACACCGATGC GCGCTGCTT	1020
GGCGCGCTCG CTGCGCGCGG GTTCACTGCC GCGCGCGCA TCGGAGCTG GATCGCGCGC	1080
GGCGCGGAGG GCGAGGTGC GCGCGAAAAC CCGACTGGT GAGTGTGGC GCGCTGTGG	1140
TAGGTGTGA TCGCTGGCG GAGGATCTC GCGCGCGGA ACGGAGTGC CGACACAGGT	1200
GGAAGTGC CCGACTGGT TCGCGCGCAA CGGCTGTG GCGCTTGGT TCGCGCGACT	1260
GCGCGATCAG CTGCGCGCGG GCGCTTGGC GAAGTTCAG CTCAAGTGC CTTACCGAA	1320
GGACCGGAGG GTACCGCGG GTCACTCTGC GCGCGGAGG AA	1360

## (3) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGACGAGCC CGATATGCG GGCACCGTAG CGAAGCGCT CCGCGAGCGA CTGCGCGCGC	60
GTATCGCTCC CTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCGGCTC	120
TGATGAGCT GCGCGCTGTT TACATCATCT ACCGCGAGCG GCGCGCGGAG CTGCGGAGCG	180
CTAAGCGCTT GCTCGGCTG CCGGACGAGT TAAAGCTGAG CTTGGCGCGC GTGACGCTAC	240
TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGCGCGCGC GCGCGAGTGC ACCGCGGAGC	300
TGATGAGCTG ATCGCGCGCG TGTGTGCGCG GCGCGGAGGA CCGATATGAG CCGCGCTCTT	360
CGAGCGCGTG GCGCGAGCG GTGCGGAGCG TATTACGCAA CTTGCAATTC CTGCGCGAAT	420
CGCGCGCTT GATGAGCTT GCGACCGAGC TGGGAGTGT CCGCGCTGT TTTGTTCTGC	480

CGATTGAGGA TTGGCTGCAA TGATCTTTG CGACGCTGGG ACAGGCCGCG GAGCTGAGC	540
GGGCTGGAGG CGGCACCGGA TATGCTTCA GCCACCTGG ACCGCGCGG GATCGGTTG	600
CCTGCACGGG CGGCACCGCT AGCGGACCGG TGTCTTTCT ACGGCTGTAT GACAGTCCG	660
CGGCTGTGCT CTGCATGGGC GTTCGCGGC GTGGCGCTG TATGGCTGTG CTTGATGTGT	720
CGCACCGCGA TATCTGTGAT TTGCTCACCG CCAAGGCGGA ATCCCCAGC GAGCTCCCG	780
ATTTCAACTT ATCGGTTGCT GTGACCGAGG CTTTCTGCG GCGGCTCGAA CGCAACGCG	840
TACACCGGCT GGTCAATCCG CGACCGGCGA AGATCGTCCG GCGGATGCGG GCGGCTGAGC	900
TGTTGAGCGC CATCTGCAA GCGCGCAGG CCGGTGGCGA TCGCGGCTG GTGTTTCTG	960
ACACGATCAA TAGGGCAAAC CCGTGGCGG GGAGAGGCGG CATCGAGCG ACCAAGCTT	1020
GCGGGAGGT CCGACTGCTG CTTACGAGT CATGTAATCT CGGCTCGATC AACTTCGCG	1080
GGATGCTGCG CGACGCTGCG GTGAGTGGG ACCGCTCGA GGAGCTCGCG GTGTGGCGG	1140
TGCGGTTGCT TGATGAGTC ATGATGTCA GCGGCTAGCG CTTCCCGGAA CTGGGTGAGG	1200
CGGCGCGCGC CAGCGCGAAG ATCGGCTGG GAGTCAATGG TTGGCGGAA CTGCTTGGG	1260
CACTGGGTAT TCGGTACGAC AATGAAGAAG CCGTGGGCTT AGCCACCGCG CTCATGCTC	1320
GCATACAGCA GCGCGCGCAC ACCGCTGCGG GGAGGCTGGC CGAGAGCGCG GCGGCATTCC	1380
CGGCTTCAC CGATAGCGCG TTGCGCGGCT CGGCGCGGAG GCGCAACGCA CAGGTGAGT	1440
CGGCTGCTCC GACGCGCA	1458

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCTGTAAAT CGTGTGGAT CTGGAACCGC GTGGCGCGCT ACCTACCGAG ATCTACTGCG	50
GCGCGAGGGG GCTGGCGGTG GGCATCGCGG TCCTCTAGT CCGGATCGCG GTGGCGATCG	120
TCATCGGCTT GGTGACAGC AGCGCGGTG CCAAAACGGT CAGCGCGGAC AAGCGCGCT	180
CGCGCGAGAG CCATCGGCGT TCGCGCGCAC CCAAGGAGC CCAGCGCGCG GCGCAACCG	240
AAGGTAACGC CGCGCGCGCG CCGCGCGAGG GCGAAACCG CGAGACAGCG ACCCGGCG	300

CCGCGGTGCA GCCCGGCGCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG	360
CCGTCAAAGG TTTGACCAAC GCGCGCGCGT ACTACGTCGG CGACCAAGCG AAGTTACCA	420
TGCTGGTCAC CAACATGCG CTGCTGTCCT GTAAACCGCA CTTTGCGCC GCGGTGTTGG	480
CGGCTTACCT TTAATGCTG GACAACAAGC GGTGTGCTC CAACCTGGAC TCGCGCGCTT	540
CGAATGAGAC GCTGCTCAAG ACCTTTTCCG CCGGTGAGCA GGTAAAGACC GCGGTGACCT	600
CGACTCGGAT GCGATCGCG CGGCGCTGCG CATTCGCGCG GCGCGCGATC GCGCGCGGCA	660
CGTACAATCT CTTGGTACAA CTGGGCAATC TCGCTGCTT GCGGTTTCCG TTGATCTGCA	720
ATCAGCGCGG GCGCGCGCGG GCGCGGCTAC CCGGTGCGCG TCGAGCGCAG GCGCGCTCCG	780
CGGAGTCTTC CGGCAAGGC GATAATTAT TGATCTGCA TGGTGGATTC CGGAGCTGT	840
GACAACCCCT CCGCTGCTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 622 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTACATGCC TCCCTGGGTG TCGAGGTGAC CAATGACAAA	60
GACACCGCGG GCGGCAAGAT GGTGCAAGTA GTGCGCGGTG GTGCTGCGCG GAACGCTGGA	120
GTGCGGAAGG GCGTCTTTGT CACCAAGGTC GACGACCGCG CGATCAGACG CCGGACCGCG	180
TTGCTTGGCG CCGTGCCTTC CAAAGCGCGG GCGCGCACCG TGGCGCTAAC CTTTCAGGAT	240
CCCTCGGGCG GTAGCGGCAC AGTGCAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAAG	300
TGCGCGCGCA GTGTTCAAAG CTCGATATA CCGTGGCACC CATGGAGCAG CCGCGCGAGT	360
TGCTGCTTGG CCGGCACTT GTCTGCTCG TTGACGATCG CACCGCGCAC GCGGATGAAG	420
AGCAGAGCGG GCGGCTTCTC ACCGAGCTCG TCACCGAGGC CGGCTTTCTT GTGACGCGCG	480
TGCTGCGCGT GTGCGCGCAC GAGGTGAGA TCGAAATGC GCTGAACACA GCGGTGATCG	540
GCGCGGTGGA CCGTGTGGTG TCGTCTGCG CGACCGGNET GACGCTGCG CATGTCACCG	600
CGGAAGCGAC CCGGACATT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGCAGCCG TAAGCCCTGT GGGGGCCCCC ACACCTGCTGT TGACAGCATG GGGCGGTGGC	60
ACCAACAGCT CTTCTCAGG CGCAGGCGGA AGCTCTGGGT GGGTGCACAG GGGCGGCAAG	120
AAGGAGCTCC ACTCCAGCG CTCGACCGCA CAGGAAATG CCATGAGCA GTTCTCTAT	180
GCCTACCTGC GATCTGCCC GGGCTACAG TTGCACTACA AGGCGACCG GTCCGTTCCC	240
GGGGTGACCC AGTTTCTCAA CAAGGAAACC GATTTCGCG GCTCGGATGT CCGCTTCAAT	300
CCCTCGACCG GTCAACCTGA CCGGTCCGCG GAGCGGTGCG GTTCCCCGCG ATGGGACCTG	360
CGGACGCTGT TCGGCCGAT CCGGATCAGT TACAATATCA AGGGCTGAG CACGCTGAAT	420
CTTGACCGAC CCACTACGCG CAAGATTTTC AACGGCACCA TCACGCTGT GAATGATCCA	480
CAGATCCAAG CCTCAACTC CGGCACGAC CTGCCGCCAA CACCGATTAG CTTATCTTC	540
CGCAGCGACA AGTCCCGTAC GTCCGACAAC TTCCAGAAAT AGCTCGACCG TGTATCCAAC	600
GGGGCGTGGG GCAAAGGCGC CAGCGAAACG TTCAGCGGG GCGTCGGCT CCGCGCCAGC	660
GGGAACAACG GAAGTCCGC CTTACTGAG AGGACCGAG GGTGATCAC CTACACGAG	720
TGGTCGTTG CCGTGGGTAA GCAATTGAAC ATGGCCGAGA TCATCAGCTC GGGGGTCCG	780
GATCCAGTGG CGATCAGGAC CGACTCGGT GGTAAAGACA TCGCTGGGCG CAAGATCATG	840
GGACAAGGCA AGGACCTGGT ATTGGACAG TCGTCTTCT ACAGACCTAC CCAGCTTGGC	900
TCTTACCGCA TCGTCTGGC GACCTATGAG ATCGTCTGT CCAATATACC GATCCGAGC	960
ACCGGTAAGT CGGTAAGGGC GTTATGCAA GCGCGGATTC GTCCAGGCGA AGAAGGCGTG	1020
GACCAATAGC GCTCCATTCC GTTGGCCAAA TCGTTCCAAG CAAAATTGGC GGGCGCGGTG	1080
AATGCTATTT CTGAGCTAG TGAAGGGAAT TCGACGTTGA GCGATGCCCT TCGCAGGTA	1140
GGGTGCGAAT TTGGGCGGTA TCAGCTATTC CGCTGCTGG GCGGAGGCGG GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

GCAAGCAGCT GCAGTGTGTC CTGTTCCGACG AACTGGGCAT GCGGAGGACC AAACGCACCA      60
AGACCGGGTA CAGCAGGAT GCGGACGGGC TCGAGTCGTT GTTCGACAAG ACCGGGCATC      120
CGTTTCTGCA ACATCTGTC GCGGACGGGC ACGTCACCCG GGTCAAGGTC ACCGTGACG      180
GTTTGTCTCA AGCGGTGGCC GCGGACGGGC GCATCCACAC CAGCTTCAC CAGACGATCG      240
CGCGGACCGG CGGCTTTTC TCGACCGAAC CCAACCTGCA GAACATCCCG ATCCGCACCG      300
ACCGGGGGCC GCGGATCCCG GAGCGTTTC TGGTCGGGGA CGGTTACCGC GAGTTGATGA      360
CGGCGACTTA CAGCCAGATC GAGATGCGCA TCATGGGCA CTTGTCCCGG GACGACGGCC      420
TCATCCAGGC GTTCAACACC GGGGAGGACC TGTATTGTTT CCGCGCGTCC CGGTTGTTCC      480
GTGTGCGCAT CGACGAGTC ACCGGCGAGT TCGGCGGCGG GGTCAAGGCG ATGTCTTACG      540
GGCTGGTTTA CGGCTTGAGC GGTACGGCC TGTGCGGCA GTTGAAAATC TCCACCGAGG      600
AAGCCACGCA GCAGATGAC GGTATTTCG CCGGATCCCG CGGGGTGCGG GACTACCTTC      660
GCGCCGTAGT CGAGCGGGCC GCGAAGGACG GGTACACCTC GACGTTGCTG GCGGTGCGCC      720
GCTACCTGCC CGAGCTGGAC AGCAGCAACC GTCAAGTCCG GAGGCGCGCC GAGCGGGCGG      780
CGCTGAACGC GCGGATCCAG GCGAGCGCGG CCGACATCAT CAAGGTGGCT ATGATCCAGG      840
TCGACGAGGC GTTCAACGAG GCACAGCTGG GTTCGCGCAT GTGCTGCGAG GTCCAGGAGC      900
AGCTGCTGTT CGAAATGCGC CGGCTGAGC GCGAGCGGCT CGAGGCTGTC GTGCGCGACA      960
AGATGGGCGG CGGTTACCGG CTGACGCTCC CGCTGAGGT GTGCGTGGC TACGGCGGCA      1020
GCTGGAGCGC GCGGCGGAC TCGTGGCGCA GGTGACATCT GCGCGCGGAA TTGCGCGATT      1080
TTTCCGCTCT GAGTTACGCG TCGGCGCAT CCGGACCGAG TTTGTCCAGC GTGTACCGCT      1140
CGAGTAGCTT GTCA
                                                                 1155

```

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GAGCGCGGTC TGGTGTGGA ACGGTTTTAC CGGTGCGCAT CGGACCGGC GTTCCCGGGT      60

```

TGGGGGCTCG	GTTTGGCGAT	CSTCAAACAG	GTGCTGCTCA	ACCACGGCGG	AFTGCTGCGC	120
ATCGAAGACA	CCGACCCAGG	CGGCCAGCCC	CCTGGAACCT	CGATTTACCT	GCTGCTCCCC	180
GGCGGTGGA	TGCGATTCC	GCAGCTTCCC	GCTGCGACCG	CTGGCGCTCG	GAGCACCGAC	240
ATCGAGAACT	CTCGGGGTTG	CGCGAAGCTT	ATCTCAGTGG	AATCTCAGTC	CACGCGCGCA	300
ACCTAGTTGT	GCAGTTACTG	TTGAAAGCCA	CACCCATGCC	AGTCCACGCA	TGGCCAACTT	360
GGCCCGAGTA	GTGGGGCTAG	TACAGGAAGA	GCAACCTAGC	GACATGACGA	ATCAGCCAGG	420
GTATTGCGCA	CGCGCGCAGC	AGCCCGGAAC	CCGAGGTTAT	GCTCAGGGGC	AGCAGCAAAC	480
GTACAGCCAG	CAGTTGCACT	GCGGTTACCC	ACCGTCCCGG	CGCCCGCAGC	CAACCCAGTA	540
CCCTCAACCC	TACGAGGCTT	TGGTGGTAC	CCGGCCGGCT	CTGATACCTG	GCCTGATTCC	600
GACCATGACG	CGCCCTGCTG	CGATGGTTCC	CGAAGCCCTT	CGTGCAGGCA	TGTTGGCCTT	660
CGCGCGCGTG	ACGATAGCGG	TGGTGTGGG	CGCGATCGGC	CGCGCGGGCG	CATCCCTGGT	720
CGGTTCAAC	CGGCGACCGG	CGGGCCCCAG	CGCGCGGCCA	GTGGCTGCCA	CGCGCGCGCC	780
AAGCATCCCC	GCAGCAAACA	TGCGGCGGGG	GTGCGTGGAA	CAGGTGGCGG	CGAAGGTGGT	840
GCGCAGTGTG	GTATGTTGG	AAACCGATCT	GGCGCGCGAG	TGGAGGAGG	GCTCCGGCAT	900
CATTCTGTCT	CGCGAGGGGC	TGATCTTGAC	CAACAACCTAC	GTGATCGCGG	CGCGCGCCAA	960
GCCTCCGCTG	GCGATCCCGC	CGCGGAAAAC	GACCGTAAGT	TTCTCTGAGC	GCGCGACCGC	1020
ACCTTTGACG	GTGCTGGGGG	CTGACCCGAC	CAGTGATATC	CGCGTCTCTT	GTGTTCAAGG	1080
CGCTCCGGGG	CTCAGCCCGA	TCTCCCTGGG	TTCTCTCTCG	GACCTGAGGG	TGCTCAGCC	1140
GCTGCTGGCG	ATCGGGTGGC	CGCTCGGTTT	GGAGGSCACC	GTGACCGCGG	CGATCTCTAG	1200
CGCTCTCAAC	CGTCCAGTGT	CGACGACCGG	CGAGGCGCGC	AACGAGAAC	CGTGTCTGGA	1260
CGCCATTGAG	ACCGACCGCG	CGATCAACCC	CGGTAACTCC	CGGGCGCGCG	TGTTGAACAT	1320
GAACGCTCAA	CTCGTGGAG	TCAACTCGGC	CATTGCGAGG	CTGGCGCGCG	ACTCAGCCGA	1380
TGCGCAGAGC	GGCTCGATCG	GTCTCGGTTT	TGCGATTGCA	GTGACCGAGG	CGAAGCGCAT	1440
CGCCGACGAG	TTGATCAGCA	CGGCAAGGC	GTGACATGCG	TGCTGCGGTG	TGCAGGTGAC	1500
CAATGACAAA	GACACCGCGG	GCGCCAAGAT	CGTGGAGTA	GTGGCGGCTG	GTGCTGCGGC	1560
GALCGCTGGA	GTGCGGAAGG	CGTCTGTTGT	CACCAAGGTC	GACGACCGCG	CGATCAACAG	1620
CGCGGACGCG	TTGGTTGCGG	CGTCTCGGTC	CAAAGCGCGG	CGCGCGCGCG	TGCGCGTAAC	1680
CTTTCAGGAT	CGCTCGGGCG	GTAGCGCGAC	AGTCCAACTC	ACCTTCGGCA	AGCGCGGAGCA	1740

GTGATSAAGG TCGCCGCGCA GTGTTCAAAG C

1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCCCG GTGCGCGCGG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC	60
ACGAGGATCC GACCTCGCAG GTTGTGGAAC CCGCCGCGCG GGAAGTATCG GTCCATGCTT	120
AGCCCGGCGA CCGCGAGCGC CGGAATGGCG CCACTGAGGA GCGCGGCAAT TTGCGCGCGC	180
CCGCGGACCG CGAGCGCGCG AATCGCGCGA GTGAGGAGCG GGGCACTCAT GCGGAGCTTG	240
ATCCAATCAA CCTGCATTCC GCGTCCGCGC CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATCG AAAACGGCGG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCGTGCCTGG	360
CGTGTGCGCT ATCAGGATGT TCTTCGCGCA AACCTGATGC CGAGGACAGG GGTGTTCCCG	420
TGAGCGCGAC GCGTCCGAC CCGCGCTCCG TCGCGGAGAT CAGCGAGTCC CTTGATCGCA	480
CAAAAGCGTT GACGAGCTTG CAGTACCGCG TCGGAACAAC CGGAAAGTC GACAGCTTGC	540
TGGGTATTAC GATTGCGAT GTGACCTCC GGGCCAATCC GCTCGCGCGA AAGGGCGTAT	600
GCACCTACAA CGACGAGCAG GTGTGCGGT TTGCGGTACA AGCGGACAAC ATCTCGGTGA	660
AACTGTTCCA CGACTGAGG AATGTCGGCT CGATTCTCGA ACTGTCAACT TCACCGCTGC	720
TGATCTCTCG CGCTCGGCTG ACGCAGCTGC TGTCCGCTGT CACGAACTTC CAAGCGCAAG	780
GTACCGAAGT GATGACCGGA ATTGCGACCA CAAAAATCAC CGGACCATC CCGCGGAGCT	840
CTGTCAAGAT GCTTGATCTT GCGCCCAAGA GTCCAAGGCG GCGGACCGTG TCGATTGCCC	900
AGGACGCGTC GCACGACTTC GTCCGAGCGA GCATCGACCT CGGATCGCGG TCGATTGAGC	960
TCACGCACTC GAAATGGAG GAACCGCTCA ACCTCGACTA GCGCGAAGTT GCGTGCAGCG	1020
GTGNTCGAA ACCCGCTTGT GAACGCTGTC AACCGNAC	1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTGGGCA CGAGAGTGA TCGACATCAT CCGGACCGGC CCCACATCCT GGGAACAGGC	60
GGCGGGCGGAG GCGGTCCAGC GCGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT	120
CATTGAGCAG GACATGGGCG TCGACAGGCG CCGCAAGATC ACCTACCGCA TCAAGCTCGA	180
ACTGTCTGTC AAGATGAGGC CGGCGCAACC GCGCTAGCAC GCGCGCGCGA GCAAGACGCA	240
AAATCGCAGG GTTTGCGGTT GATTCTGCGG ATTTTGTGTC TGCTCGCGGA GCGCTACGAG	300
GCGCGCGGCA GTTCGCGGTC CTGCGGTATC CAGCGGTGCA TCGCGATTCC GCGCGCGGAG	360
CGGAGTTAA TCGTTGCGGT CGACCTGAAC TCGCGGATCC GCGCGGAGGC TGATCGATGA	420
CGTTGCGGAG CCGCTCGATG CCGGAGTTGC CCGAGGAAAC GTGCTGCGAG GCGGCTAGGA	480
AGCGTCGCTA GCGCGCGGTC CTGACCGGCT CTGCGTGCAC CTCAGTGCAG GCCAGCGGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCGGCG GCGCGCTCGG TTGCGCGCAT TCGCGCGGTC GCGGATCAGC TCGCGATCGC	60
CAGCATCACC GCGTTGCGCG CCGGACCGCG CCGTGGCGCG GGGGCGCGCG ATGCGACCGC	120
TTGACCGTGG CCGCGCGGCG CCGGATTCGC ATACAGCACC CCGCGCGCGG CAGCGTTACC	180
GCGGTGCGCA CCGTGGCGCG CCGTGGCGGT TCAGCGCGCG GAGCGCGAAT GAACCGCGCG	240
CAAGCGCGCG GCGGCGCGCG TTGCGCGGTT TTGCGCGCGC CCGCGCGCGC CCGCGAATTC	300
CGGACAGCGC AAGCAGCGGT GCGGCGCGCG CCGCGCGCGT TAAGCGCGCT GCGGCGCGCG	360
GCGCGCGGAC CCGCGATTAC CCGCGTTGCG GTTCGCGTGC CCGCGGTAC CCGCGCGCGC	420
GTTCGCGCGC AATATTCGCG GCGCAGCGCG AGACCGCGCG GCGCGACCAT TCGCGCGCGG	480
CACCGAAGCA ACAGCGCAAC GTGCGCGCGG GCGCGCGCGT TTGCGCGCAT CACCGCGCAT	540
TCAGCGCGAG CAGCGCGGT AATGTTTATG AAGCGCGTAC CCGCAGCGCG CCGCGTATTC	600
CGCGCGCGCG GAGCGCGTGC CCGCGCGCGC CCGCAGCGCG CAAAGCGCGG GCGTTGCGCG	660

CGGCCCCCGCC GGACCCACCG GTCCCGCCGA TCCCCCGTT GCGCCCGGTG CCGCCGCCAT	726
TGCTGCTGCT GAAGCCGTTA GCGCCCGTTC CGCAGGTTCC GCGCGTGGCG CCNTGGCGGC	786
CGGCCCCCGCC GTTGCCTAC AGCCACCCCG CGTGGCGGCC GTTCCCGCCA TTGCCGCCAT	846
TGCGCCCGTT GCGGCCATTG CCGCCGTTCC GCGCCCGACC GCGCGGTTGG CCGCCCGCGC	906
CGCCCGCGGC CGC	913

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GTTAGAAAA ATCTGCGGC CCGGACCCCTT AAGGCTGGGA CAATTTCTGA	60
TAGCTACCCC GACACAGAG GTTACGGGAT GAGCAATTCC CGCCGCGCT CACTCAGGTG	120
GTGATGCTTG CTGAGCGTGC TGGTGGCGT CCGGCTGGGC CTGGGACGG CGCCGCCCCA	180
GGCGGCCCCG CCGGCTTGT GCGAGGACCG GTTCCGCGAC TTCCCGCGGC TCGCCCTCGA	240
CCCGTCCCGC ATGGTCGCCC AAGTGGCCCC ACAGGTGGTC AACATCAACA CCAAACTGGG	300
CTACAACAAC GCGTGGGCG CCGGAGCGCG CATGCTCATC GATCCCAAGC GTGTCTGCT	360
GACCAACAAC CAGCTGATCG CGGCGGCCAC CGACATCAAT CGGTCAGCG TCGGCTCGCG	420
CCAAAGCTAC GCGTGGATG TGGTGGGTA TGACCGGACC CAGGAGTCC CGGTGCTGCA	480
GCTGCGCGGT GCGGTGGCC TGCGTCCGC GCGCATCGGT GCGGGGCTCG CGGTGCTCA	540
GCGGCTGCTC GCGATGGCA ACAGCGGTGG GCAGGCGCGA AGCGCGCTG CGGTGCTGG	600
CAGGCTGCTC GCGTGGGC AAACCTGCA GCGTGGGAT TCGTGACCG GTGCGGAGA	660
GACATTGAAC GCGTTCATCC AGTTCGATGC CGCAATCCAG GCGGTGATT CCGGCGCGCC	720
CGTCTCAAC GCGCTAGGAC AGGTGCTCG TATGAACAG GCGCGCTCC ATAACCTCCA	780
GCTGTCCGAG GGTGGGCGG GATTGCGCAT TCGGATCGGG CAGGCGATGG CGATCGCGCG	840
CCAAATCGGA TCGGTGGGG GGTACCCAC CTTTCATATC GGGGCTACCG CTTTCTCGG	900
CTTGGGTGTT GTGACAACA AGGCAACGG CCGACGAGTC CAACCGCTGG TCGGAGCGC	960
TCCGCGCGCA AGTCTGCGA TGTCCACCG CGACGTGATC ACCGCGCTCG ACAGCGCTCC	1020

GATCAACTCG GCCACCCCGA TGGCGGACGC GCTTAAACGG CATCATCCCG GTGACGTGAT	1080
CTCGGTGAAC TGGCAAAACA AGTCGGCGCG CACCGGTACA GGGAACTGA CATTGCCCGA	1140
GGGACCCCGG GCCTGATTG TCGCGGATAC CACCGCCCGG CCGGCCAATT GATTTCGCG	1200
CAGCCGTGAT TCGCGGTGA GCGCCCGAGT TCGGTCTCCC GTGCGCGTGG CATTGTGGAA	1260
GCAATGAAC AGGCAGAACA CAGCTTGAG CACCGTCCC TCGAGGGCAG TTACTCCAA	1320
GGCGGTGTGG TCGAGCATCC GATGCCAAG GACTTCGCA GCGCGCGCG CCTGCCCCCG	1380
GATCCGACCT GGTTTAAGCA CCGCTCTTC TACGAGGTGC TGGTCCCGGC GTTCTTCGAC	1440
GCGAGCCCGG ACGGTTCGCG GATCTGCTT GACTCATCG ATCGGCTCA CTACTTCAG	1500
TGGTTGCA TCGACTGAT CTGTTCCCGC GTTCTTACG ACTCAGCGT GCGCGACGG	1560
GTTTACGCA TTCCGACTT CTACAAGTG GTGCGGCAAT TCGGACCGT CGACGATTC	1620
GTGCGCTGG TCGACACCG TCACCGCGCA GGTATCGCA TCATCAGCA CCGGTGATG	1680
AATCAGACT CGGAGTCCA CCGTGCTTT CAGGAGTCC GCGCGACCG AGACCGACCG	1740
TACGTTGACT ATTACGTTG GAGCGACAC AGCGAGCGT ACACGAGCG CCGGATCAT	1800
TTCGTCGCA CGGAGAGTC GAACTGCTCA TTGATCTCG TCGCGGACA GTTCTACTG	1860
GCACCGATTC TT	1872

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGGCGGAA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGAGG GGTTCGAC	60
CCGCGCTGCT CCGCGAGATC AGCGAGTCC TTGATCGGAC AAAAGCGTTG ACCAGCTGCG	120
ACGTAGCGGT CGGAACAACC GGGAAAGTCC ACAGCTTCTT GGTATTACG ACTCGGATG	180
TGGAGTCCG GCGCAATCCG CTGCGCGCAA AGGCGGTATG CACCTACAGC GACGAGCAGG	240
GTGTCCCGTT TCGGTACAA GCGGACAACA TGTGCTGAA ACTGTTGAC GACTGGAGCA	300
ATCTCGGCTC GATTCTGAA CTGTCAACTT CAGCGTCTT GATCTCTCC GCTGGGTGA	360
CGCAGCTGCT GTCCGCTGTC ACBAACCTCC AAGCGCAAGG TACGGAAGTG ATAGACGGAA	420
TTTCGAGCAC CAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG GTGATCTCG	480

GGCCCAAGAG TCAGAGGCGG GCGACCGTGT GGATTCGCGA GGACCGCTCG CACCACCTCG	540
TCCSAGCGAG CATCGACTTC GATTCGGGT CGATTCAGCT CAGCGAGTCG AAATGGAAAG	580
AACCCCTCAA CTTCCACTAG GCCCAAGTTG CCGTCAGCGG TTGCTCGAAA CCGCTTTGTG	620
AACGCTGTCA ACGGCACCGG AAAACTGAGC CCGTCAGCGG ATCTGAAAT TCACCCCTTA	720
GACCGGCGCG TTGCTGTGA TTCTTCGGTG GTTCGCGTG GTGGGACCGG GCGGAGTTCG	780
CGCTCTTTGA GCGGTAGCT GTCCCTTTG AGGGCGACGA CTTGAGCATG GTGGACGAGG	840
CGCTCGATCA TGGCGGACG AACGAGTTCG TCGCGCGCGA AAACCTCGCG CCACCGCGCG	900
AAGGCTTAT TCGAGTAC GATCAAGCTG GCGCGCTCAT ACCCGGAGGA CACGAGTTCG	960
AAGAAGAGGT TCGCGCGTC GCGTCAAGC GGAATGTAAC CGACTTCGTC AACCGCAGG	1020
AGCGGATAGC GCGCAAGCTG GTGAGTTTC GCGTAGATGC GCGCGCGCTG GTGAGCTTCG	1080
GCGAAGCTG CTACCGATTC GCGCGCGCTG GCGAAGACGA CCGGATGACT GCGCTGACAC	1140
GCGGTATCG CCAGGCGGAC CGCAAGATGA GTCTTCGCGG TCGGAGGCGG GCGCGAAAAA	1200
CACGAGTTA TCGCGCGCGG TGATGAAATC CAGGCTGCGG AGATGTGCGA TGCTGTGCGG	1260
TTTGAGGCGA CGAGCATGCT CAAGTGGAA CTCTTCGAA CACTTCGAA CCGGAAAGCG	1320
GCGCGCGCGG ATCGCGCTT CACGAGCTG CGACTTCGCG GCTGACACTT CCGCTTCAG	1380
GCGCGCGCGG AGTATCTTT CCGGCTTCA GTCTCGCGG CCGGCGCGAT CCGGAGCGG	1440
CGACACTGAC TCAGCGAGG TCGGAGCTTT CATGCTCTT GT	1482

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGCGA CGAGCGCGCG ATAGCTTCTG GCGCGCGCGG GACGAGATCG CTGAGGCTT	60
GTGCTTCGCG GCGACCGCGG GCGGACCGAC CCGGACCGGT GAGGCGCTGC AACCGCGGA	120
CGTCACTTCG TTGCTGCTCG ACGGACCGAA CCGGCGCGTG GTTGGCTACG ACCCGGCTT	180
CGCTACGAA ATCGGTACA TCGGGAAG CCGACTGCGG AGGATGTGCG GCGAGAACCC	240
CGAGAACATC TTCTTCTACA TCAGCTCTA CAACGAGCGG TACGTGCGG CCGCGAGCG	300

GGAGAACTTC GATCCGAGG GCGTGTCTGG GGGTATCTAC CGTATCACC CGGCCACCGA 360  
 GCAAGCCACC AACAGGNC AGATCCTGGC CTCGGGGTA GCGATGCCCC CGGCGCTGCG 420  
 GGCAGCAGAG ATGCTGGCCG CCGAGTGGGA TGTGCGCGCG GACGTGTGT CCGTGACCAG 480  
 TTGGGCGCAG CTAAACCCCG ACCGGGTGCT CATCGAGACC GAGAAGCTCC GCCACCCCGA 540  
 TCGGCGCGCG GCGGTGCGCT ACCTACAGAG AGCGCTGGAG AATGCTCGGG GCGCGGTGAT 600  
 CGCGGTGTCC GACTGATGCG GCGCGGTCCC CGAGCAGATC CGACCGTGGG TCGCGCGCAC 660  
 ATACCTCACC TTGGGCACCG ACCGGTTCGG TTTTTCGGAC ACTCGGCCCC CGGCTCGTCC 720  
 TTACTTCGAC ACCGACCCCG AATCCAGCT TGTGCGCGT TTGGGAGGG GTTGGCGCGG 780  
 TCGACGGGTC AATATCGACC CATTCGCTCC CGGTCTGGCG CGGCGCGCGG AGTTACCCCG 840  
 ATTGACGAA GTTGGGGGCT TCGCGCGCGG TAAGTT 876

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGCG GCTGCAGAA TTGGGCACGA GAGACAAAT TCCACCGCTT AATGCAGGAA 60  
 CAGATTGATA ACCAATTGAC AGCGGCACAA CAATATGTCC CGATCCCGGT TTATTTGAC 120  
 AGCGAAGACC TCGTCCAGTT GCGGAAGCAT TTTTACAGCC AAGCGGTGCA GGAACGAAAC 180  
 CATGCAATGA TGTCTGTGCA ACACCTGCTC GACCGCGACC TTGCTGTGCA AATTCCCGCG 240  
 GTAGACACCG TCGGAAACCA GTTGCACAGA CCCCCTGAGG CACTGCGGCT GCGCTCGAT 300  
 CAGGAACGCA CAGTCACCGA CCAGGTGCTT CGGCTGACAG CGGTGGCCCC CGACGAGGCG 360  
 GATTTCTCTG GCGAGCAGTT CATGCACTGG TTCTTGCAGG AACAGATGCA AGAGGTGCCC 420  
 TTGATGGCAA CCTGTGTGCG GTTGGCGCAT CGGCGCGCGG CCAACGTGTT CGAGCTAGAG 480  
 AACTTCGTCC CAGCTGAAGT GGATGTGCGG CCGGCGGCAT CAGGCGCGCG GCACGCTGCC 540  
 GCGGCGCGCG TCTAGATGCG TGGGCGGAT CAGCGAGTGG TCCCGTTGCG CCGCGGTGCT 600  
 TCCAGCGAGG CTTTGTGCG GCGGCGGTGG TGAATACCA TCCAGGCGAC CCGGACCTCC 660  
 CGGNAAGAT CGATGTCTTC GTACTCATCG ACCTTCCAGG AGTACACCGC CCGGCTCTGA 720  
 GCTGCGGAGC GTTCAACGAG TTGCGGATAT TCTTTTAAAG CAGGCACTGA GGTGCGGAGC 780



```

GCGGTTGGCC CGACCCGCGT GCGCGCACTG CTGGTCAGGT ATCGCGGGGT CTGCGCGAGC      840
AACCAACGTG GCAGGAGGGG TCGACCCCGC CGGATCGCA GACCGGGGGG GCGAAAACGA      900
CATCACACCC GCACCGGATC GATCTGCGGA GGGGGGTGCG GGAATACCGA ACCGGTGTAG      960
GAGCGCCAGC AGTTGTTTTT CCACCAGCGA AGCGTTTTCG GGTTCATCGG GCGNNTTAAG     1020
T                                                                                   1021

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

CGTGGCGAGC AACCGAAGAA CACAACCATG AAGATGCTGA AATCGATCGC CGCGGTCTG      60
ACCGCCGCGG CTGCAATCGG CCGCGCTGCG GCGGTGTGGA CTTCGATCAT GCGTGGCGGN     120
CGCGTCGTAT ACCAGATGCA GCGCGTCGTC TTGCGCGCGC CACTGCCCTT GGACCCCGNA     180
TCCGCCCCCTG ANGTCCCGAC CCGCGCCGAG TCGACGAGNC TCGTCAACAG NCTCGNCGAT     240
CCCAACGTGT CTTTGTGAGG CAAGCGNAGT CTGGTCGAGG GNGGNATCGG NCGNANCGAG     300
GCGNGNATC GNCNANCA A
                                                                                   321

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

TCTTATCGGT TCGGTTGGC GACGGCTTTT GGNGCGGGT GGTAAACCG CTGCGCCAGC      60
CGATCGACGG GCGCGGAGAC GTGACTCGG AACTCGGCG CCGCTGAGG CTCCAGGCGC     120
CCTCGGTGGT GNACCGGCA GCGGTGAAGG AGCGTTGNA GACCGGATC AAGCGATTC     180
ACCGATGAC CTGATCGGC CCGCGCGAGC GCGAGCTGAT CATCGGGAC CGCAAGACCG     240
GCAAAAACCG CCGTGTGTGT CGGACACCAT CTCRAACCA GCGGGAAGAA CTGGGATTC     300
GGTGGATCGC AAGAGGAGG TCGCTTTGTG TATACGTTGG CCATCGGCGA AGAAGGCGAA     360

```

CTTACCATCG CCG

373

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCCT GATGGGATTC CTGGGCGGGG CCGGTCCCTT GCGGTGGGTG GATCAGCAAC	60
TGTTTACCCG GGTGCGGCAA GCTGTGTCCT TTGCTCAGGC AGCGGTGTG CCGGTGCTCT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAGGCGGGGC GAATCGGTGC	180
TGATCCATGC CGGTACCGGG GGTGTGGGCA TGGCGGCTCT GCAGCTGGCT CGCCATGGG	240
GCCTGGAGGT TTTGCTCAGC GCCAGCGGTG GNAAGTGGGA CACGCTGGGC GGCATGNGT	300
TTGACGACGA NCCATATCGG NGATTCCGNC ACATNCGAAG TTCCGANGGA GA	352

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCGGGC TTGATTCCCT TCGACGAGCG GGTGGGATA ATCGAGGAAG TGATCAGCC	60
GCGGTTCGGC GCGGTCTATG GTACAGCGA GTAATCAGCA AGTTCTCTGG TATATCGCAC	120
CTAGCGTCCA GTTCTTTGCC AGATCGCTTT GGTACCTCA TCGCATGTAC CGGTTCGGCT	180
GGCCGACGCT CATGCTGGCG GGTGCTATCC TGGCCAGGG TGTGGCGGCT CTCGGGGTCG	240
GGCGCGAGTC CGCAGCCCAA ACCGCGCGCG TGGCGACTA CTACTGCTGC CCGGGGCAGC	300
CTTTGACCC CGCATGGGGG CCGAAGTGG ATCCCTACAC CTGCCATGAC GACTTCGACC	360
GCGACAGCGA CCGGCGCGAC CAGAGCCGCG ACTACCGCG ACCCATCTC GAAGTCCCG	420
TGCTTACGA TCCCGGTGCT GCGCGCGCGC CCGCGCTGC CGTGGCGGC GCATAGCCT	480
CGTTTACCG GCGCATCAG CGAATACCG TATAAACCG GCGTGGCGC CGGCAAGTA	540
CGATCGCGCG CCGGGCAGAT TTACGCTGCG GTGCGATCG ATCGCGCGCT CCGATGACAG	600
AAAATAGCG ACCGTTTTGG CACCGCTTG GAGGACGCTT GAAGCGAACC TGTGATGAAC	660

GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCGGCACACC CGTTCCCGCG 720  
ATCGTG 726

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGAGC AGGAACGTGC GAGCCACAC CCGCTATGCC TTGATGCAGG CGACCCGGAT 60  
CGTCGCCGAC CATATCCAAG CATGCTGGGT GCGGACTGAG CGACCTTTTG ACCAGCCCGG 120  
CTGCCCCGATG GCGGCCCCGT GAAGTCATTG CCGCGGGGCT TGTGCACCTG ATGAACCGCA 180  
ATAGGGARCA ATAGCGCGGT GATTTCGAG TTCAATGTCC GGTATGGCTG GAAATCCAAT 240  
GGCGGGGCAT GGTCCGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCCA ATCTGGAGGG 300  
AGCAATCAAT GCGGCGGATG AAGCCCCGGA CCGCGGACCG TCCTTTGGAA GCAACTAAGC 360  
AGGGCGCGCG CATTTGATG CCACTACCA CTTAGGGCTG CGTCCGCTG GTCTCGAGC 420  
TGACACCCGA CGAAGCGGCG GCACTGGGTG ACCAACTCAA AGCGCTTACT AGCTAAGACC 480  
AGCCCCACCG CGAATGCTG GCTTACCGG CACACCTTCG GGTAGATGTC CAGTCTCTGC 540  
TGGGCGATGT ATGCCGAGGA GAAGTCTTGG ATACAGGCT 588

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGTTTT TGGCGGGGCG GGGGCGGTGC GCGGCAACCG CCGGCGGGC 60  
GGTACCCCGG GGTGTTTCGG TGTGGCGGG GCGGTGGGG CCGGAGGCAA CGGCATGCG 120  
GCTGTCACCG GTACGTGCGC CAGCACACCG GGTGGATCC 160

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTCCACA CCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCGC CGTTCGCGGA GCGCGCTGCC	120
AAGGCGATGG GAATCGACAA GCTGCGGCTA ATTCTACCG GAATCGACCG GCTCGTGGCT	180
GAACGCGAAC AGTGGGACGA CCGCAACAAC ACCTGGCGT TGGCGCGCG TGTGGTTGTC	240
GCCTACGAGC CCAACGTACA GACCAACGCT CG	372

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCGGCTG GTTCTCGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CCGGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCTGCGCG GGTTCATCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGTTCATCG GGTGAGCGCG GCGACGATCC	180
GTTGCGATCT GCGTGGCTTC GAGACGCTCT ATTCTGACA TCGCTGCGC GCTGCTGCG	240
GGAATCTGAC CCGAAGATG AAGAGCGCT CAAAGATCCA CGTCTCGAC AGTGGCTTCC	300
CGGCTGCTT GCGCGCG	317

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTGATGA ACACCGTTC CCGACGCGC GCGGCCAGCA CTTGGTGTGA	60
GCAGCGCGCG ACCACCTCGC CGTGGGCGG CATGGTGATG ACCACCTCGC CTTGGGCGAC	120
CGCTTGGGCG GCGTACGAA ACACCGGAC ACCGTGCGC GCGCGCGCG ACBCCGCTGT	180
CG	182

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GATCGCGAAG TTTGGTGAGC AGGTGGTCGA CCGGAAAGTC TGGCGGCTG CGAAGCGGCT    60
CGCGGTTTAC GAGGCGAAGA CAGCGCTGTC CAGCTGCTG CGGCTCGTCT ACGGCGGGCA    120
GAGGTTGAGA TTGCCCCCCC CCGCGAGCCC GTAGCAAAGC TTGTGCGGCT GCATGCTCAT    180
GAGACTCGGC GGTTAGGCAT TGACCATGGC GTGTACCCGC TCCCCGACCA TTTGGAGGCT    240
CGGTTGTCAG ACCAGCTGCT CCAACGCTTT CACCGGTGAA GCGCTAGCTC ATCGACAGCC    300
ACGTTTGG                                         308

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

CCGACGACCA GCACTCACC TGATCATGG TCGGCAGCG CATTGAGGAC GGAGAGAATC    60
CGGCCGAAGC TCCCCGCGCG CAGTGTCTCA TACTGACCGG CGTAGAGCG CTCCCCCGAT    120
GGCACCGGAC TATTCTGCTG TCGGCTGGC CGGTAAGAGC GGGTAAAGA ATGTGAGGGG    180
ACACGATGAG CAATCACACC TACTGAGTGA TCGAGATGCT CCGGACTTCC CCGGACGGCG    240
TGGACCGCGC AATCCAGGGC GGTCTGG                                         267

```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

CTGTTGCCGA AAGAATGTGA GGGGACACCA TGAGCAATCA CACCTACCGA GTGATCGAGA    60
TCTTCGGGAC CTGCCCCGAC GCGTGGAGC CGGCAATCCA GCGCGGTGTG GCGCGAGCTG    120

```

CGCAGACCAT	GGGCGCGCTG	GACTGGTTCC	AAGTACAGTC	AATTCGAGGC	CACCTGGTCC	180
ACGGAGCGGT	CGCGCACTTC	CAGGTGACTA	TGAAAGTCGG	CTTCGGCTGG	AGGATTCTCC	240
AACCTTCAAG	CGCGGCGGAT	AAGTGAGGTG	CATCATTAAG	CGACTTTTCC	AGAACATCCT	300
GACGCGCTGG	AAACCGCGTT	CAGCGGACGG	TGGCTCGGCC	GAGGCGCTGC	CTCCAAAATC	360
CCTGCGACAA	TTGGTCGGCG	GCGGCTACAA	GGAAGTCGGT	GCTGAATTCC	TGGGTATCTT	420
GGTGACCTG	TGTGGGCTGC	AGCGGACGA	AGCGTCTCTC	GACGTGGGCT	GGCGCTCGGG	480
GCGGATGGCG	TTGGCGCTCA	CGGCTATCT	GAACAGCGAG	GGACGCTACG	CGCGCTTCSA	540
TATCTCGCAG	AAAGCCATCG	CTGGTCCCA	GGAGCACATC	ACCTCGGCGC	ACCCCAACTT	600
CCAGTTCCAG	GTCTCCGACA	TCTACAACTC	GCTGTACAAC	CCGAAAGGGA	AATACCACTC	660
ACTAGACTTT	CGCTTTCCAT	ATCGGATGC	GTGTTGGAT	GTGGTGTTC	TTACCTCGGT	720
GTTCACCCAC	ATGTTTCGGC	CGGACGTGGA	GCACTATCTG	GACGAGATCT	CGCGCGTGGT	780
GAAGCCCGGC	GGACGATGCC	TGTGCAGSTA	CTTCTTCTCT	AATGACGAGT	CGTTAGCCCA	840
CATCGCGGAA	GGAAAGAGTG	CGCACAACTT	CCAGCATGAG	GGACCGGCTT	ATCGGACAAAT	900
CCACAAGAAG	CGGCGCGAAG	AAGCAATCGG	CTTSCCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCTTCGCGG	TGCACGAACC	ATTGCACTAC	GGCTCATGGA	GTGGCGGGA	1020
ACCACGCGTA	AGCTTCAGG	ACATCGTCAT	CGGACCCAA	ACCGCGAGCT	AGGTGCGCAT	1080
CCGGGAAGCA	TGGGACACT	GTGGGCGGA	GGCGCGCTGC	CGGAGGCGG	ATTAGGCGGG	1140
CAGATTAGCC	CGCGCGGCT	CGCGGCTCG	AGTACCGCGC	CGCGAATGGC	GTACCGGCGT	1200
GGAACCAAG	CTTGGCGCGG	TGGGCGCGCG	CCTGCGGAT	CAGGTGGTAG	ATGCGGACAA	1260
AGCCTGCGTG	ATCGGTCAATC	ACCAAGGCTG	ACAGCAGCGG	GTGTGCACT	AGCGCGAAGG	1320
CCACCCCGGT	CTCGGGGTCT	GTCCAGCGGA	TGAGCGCGG	CAAGCGGACA	TGACCAAGCC	1380
CGCGCATCAC	GTTCGGGATC	GGCATACCGT	GATAGCCAGG	ATGAAAATTT	AAGGGCACCA	1440
ATAGATTTCC	ATCGGCGAGA	ACTTGGCGTC	GCTTGGCGGT	CAGCGCGCGT	ACCAGCTCCC	1500
GCGACAAGAA	CGGTATGCGG	TGATCTCGC	CTGCTGCGG			1519

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

CTCCAGGGTG GCTTGGAATGA GGTTCACCGC GGGGCAGGCC GAGTTGACCT CCGCCCAAGT    60
CCGGGTTTCT GCGGCGGCTT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT    120
CCTCGAGAAC CTGTCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GCAAAACAC    180
CCCGCGCATC GCGGTCAACG AGGCCGAATA CCGCGAGATG TGGGCCCAAG ACCGCCCGGC    240
GATGTTTGGC TAGGCCCGCG CAGCCGCGAC GCGACCGGCC ACGTTGCTGC CGTTCCAGGA    300
GGCCTCGGAG ATGACCAGCG CCGGTGGGCT CTTCCAGCAG GCGGCGCGCG TCGAGGAGGC    360
CTCCGACACC GCTCCGCGCA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAAACAGTT    420
GGCCAGCGCG ACGCAGGGCA CCACGCTTC TTCCAGCTG GGTGGCCTGT GGAAGACGCT    480
CTCGCGCAT CCGTCGCGCA TCAGCAACAT GGTGTGATG GCCAACAACC ACATGTGAT    540
GACCAACTCG GGTGTGTGCA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTGC    600
GGCGCGCGCG GCGCAGGCGC TCAGAACCGC GCGGCAAAAC GCGGTCCGCG CGATGAGCTC    660
GCTGGGCGAG TCGTGGGTT CTTGGGTTCT GGGCGTTGGG GTGGCGCGCA ACTTGCTCG    720
GGCGCGCTCG GTACGGTATG GTACCGGCGA TGGCGGAAAA TATGCANAGT CTGGTCCGCG    780
GAACGGTGGT CCGCGTAAG GTTACTCGC GTTTCTGGA TCGGTGAAC TTGTCAAGC    840
GAAACAGTTA C                                     851

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GATCGATCGG GCGGAAATTT GAGCCAGATT CGCTCCGCG GATAACCCAA TCAATCGAAC    60
CTAGATTAT TCGTCCAGG GCGCCGAGTA ATGGCTCGCA GGAGAGGAAC CTTACTGCTG    120
CGGSCACCTG TCGTAGGCTC TCGATACGCG GGAAGGCGTC GACATTTTCC ACCGACACCT    180
CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGACCGAGT CGCAGGCTCG    240
GCTTGGTCAA GATC                                     254

```

(2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GATCCTGACC GAAGCGGCCC CGGCCAAGGC GAATTCGCTG TTGGACCCAG AGGGACGGGA      60
CGATCTGGCG CTCGGGATCG CGGTTGAGCC GGGGGGGTGC GCTGGATTGC GCTATAACCT      120
TTTCTTCCAC GACCGGACGC TGGATGGTGA CCAAACGGCG GAGTTGGGTG GTGTGAGTTC      180
GATCGTGGAC CGGATGAGCG CGCCGATATG GGAAGGCGCG TCGATCGATT TCGTCCACAC      240
TATTGAGAAG CAAGGTTTAC CATCGACAAT CCGAACGCCA CCGGCTCCTG CGCGTCCGGG      300
GATTGGTTCA ACTGATAAAA CCTAGTACG ACCCGCGCGT GCGCAACACG TACGAGCACA      360
CCAAGACCTG ACCGCGCTGG AAAAGCAACT GAGCGATGCC TTGCACCTGA CCGCGTGGCG      420
GGCGCGCGCG GGCAGGTGTC ACTTCGATGG TGAACAGCAC CTGGGCGTTG TATTGCGACC      480
AGTACACGAT TTTGTCCATC GAGGTGACTT CGAGCTGGGA GAAGTGGTTG CCGAACGGCT      540
CGCTGCTCAG CTTGCGCAAG CCTTGATCGG AGCGCTTTTC GCGCACGCGG TCGTGGATAC      600
CGCACAGCGC ATTGCGAAGC ATGTTGTCCA CATCGCGTTT CTCCAGCGCG TTGAGGTATC      660
CCTGAATCGC GGTTTTGGCC GTTCCCTCCG AGAATGTGCC TCGCGTGTTC GCTCCGTTGG      720
TCCCGACCCC GATATCGATC GCGCGCTTCA TAGCCGACAC CAGCGCGAGG CCTACGACAA      780
TCCCGATCAG CAGCGCGTTG TCGCGTCCGT TCGGCTAGGA CACTGCGGC GGCACGCGCG      840
GATATGCGCG GCGCGCGAGC GCGCGCTCCT CTGCGGCTCC CCGGGCGAAG GCGCGTTCCG      900
CGCGCGCGAG GTCTTGGGGG TAGTCCAGCG CTTCGCGTTC GTGGGATGAG GGCTCGGSGT      960
ACCGCGCGCG TCGTTTGGTG CCGACACCGG GGTTCGCGCA GTGGGACCG GCGATTGTGG      1020
TTCTCCTAGG GTGGTGACG GGACCAAGTG CTAGGGCGAC AACCGCCCGT CGCGTCAGCG      1080
GCGAGCATCG GCAATCAGGT GAGCTCGTTA GCGAGGCTAG CCGACAGCT GCGGTGAGCT      1140
CTCAACGCGA CCGGGCGCGC CCGCGCGCGG ATAATGTTGA AAGACTAGGC AACCTTAGGA      1200
ACGAAGGACG GAGATTTTGT GACGATC

```

## (2) INFORMATION FOR SEQ ID NO:36:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCCG CGGATCCGCG GGGTGGTTGA ACCGCAACGG CCGGCCCCCG GGGCCCCGCG	60
GGACCGGGCG TAACGGTGGT GCGGCGCGCA ACAGCTGGTT GTTCGGGGCC GCGGGTCCG	120
GCGGCGCGCG CACCAATGGT GGGTCCGCGG GTTCGGGGCG ATTGTCTAC GCGCAACGCG	180
G	240

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCCG CGGATCCGCG GGGTGGTTGA ACCGCAACGG CCGTGTCCCG GCGCGGGCG	60
GCGACCGCGT GTTCCCGGCT GCGGCGCGCG AGGGCGGCTT CGGTGGCGAG GCGCGCAATG	120
GCGGCGCGCT CACCGCGCGG AACGCGCGTC TTGGCGCGCG GCGCGGTGGC GGAGGCAACG	180
CGCGGACCGG CGGTTTCGCT GCGACCGCGG GTAAGGTTGG CAGGCGCGGN ATTGGCGCGC	240
GCATCGAGAG CCGGACCGCG CTCGCGGCTG ACCGCGGTGA CCGCGGTGAC	290

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCACTGG CATCGGCGGT GTCACTCGAA GCAT	34
---------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GATGGTGGCT CCGCCCCCCC TTCCCGCCGA CCGCACCCTT CCCACGTTA CCGAACAAGC      60
TGGCGTGGTC GGCAGCAGCC CGGCGACCGC CGACGCGGA GTCGAACAAT GGCACCGTCC      120
TATCCCCACC ATTSCCGCCG GNCDCACCGG CACCG                      155

```

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

ATGGCGTTCA CCGGCGCCCG GGCACCGGC AGCCCGGCG GCGCGCGCG TCG      53

```

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GATCCACCGC CGGTCCAGAC GGTCCCCCG GCGCCACCTT GACCAGCGGC GGCACGCGC      60
GCACCGCGCG CACCGCGCG AACCCACCG TGTCTCGCG GCGCGCGCG GCGCGCGCG      120
AGCGCGCGCA CG                      132

```

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

GATCGCGCGC CGGACCGCG GCGACCGCG GCAAGCGCG AACCGCGCG GCGGACGCA      60
CGCGCAAGA ATCTTCCCG TCNCCAATC GCGGGAATG CCGACAGCG GCGAAGCGC      120
GCACGCGCG CA                      132

```

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGGTGCGG ATTGCGCGGG TTTCGCCACG	60
CGAGGAAAGC CGGTACGAGA TGCGCTGCGG GAACTAGGCG GATCCGTTGG CGATGCCCGG	120
ATGAACGGGG GGCATCAAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGCGTAT	180
AGCACTAAGG AGGATGATCG GATAAGACCG AGTCCGAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGCCCAAC GAGGTGGAGG CCGCGATGGC GGACCCAGCG ACTGATGTTC	300
CGATCACAAT GTCCGAATTC ACGGCGGNTA AAAACGCGCG CCAACAGNTG GTNTTGTCCG	360
CGGACAACAT GCGGGAATAC CTGCGCGCGG GTGCCAAGA GCGGCAGGCT CTGGCGAATT	420
CGGTGCGCAA CGCGGCCAAG GNGTATGCGG AGTTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACCG CGAAGGAAT GTGCAGCCAG AATCGGCGCG GGCGGTGCGA CGGCGACATT	540
CGGCGGAAT AACCGATACG CCGAGGGTGG CGACGCGCGG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GCGAAGGAAG CTCGAAACCG GCGACCAAGG CGCATCGCTC GCGCACTGNC	660
CGGATGGGTG GAACACTTNC ACCCTGACCG TGCAAGGCGA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCTGCAG CGCTGTGCGG CGACGTGCGG GTCAAAGCGG CATCGCTCGG TGCGCTGCGA	60
GGCGCGCGGG TGCGCTGCGG GCGCTTGGGA TCGCGGATCG GCGCGCGCGA ATCGGTGCGG	120
CGCGCTGCGG CTGCTGACAT TGCGCGCTTA GCGCAAGGAA GCGCGCGCGG CGCGCGCGCG	180
CTGGCGCGCG GTGCGATGCG AATGCGGATG GTGCGCGCGG ATCAGGCGAC AGGGGCGCGC	240
AAGTCCAAGG GTTCTGAGCA GGAAGACGAG GCGCTGTACA CCGCGGATCC TGCTGCGG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1058 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG ATCGAATGCG GTGCGCGGGA GCACAGCGTC GCACTGCACC AGTGGAGGAG	60
CCATGACCTA CTCGCGGGGT AACCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTGCTACG	120
GAGGCGTCAC ACCCTCGTTC GCGCACGCGC ATGAGGGTGC GAGCAAGCTA CCGATGTACC	180
TGAACATGCG GGTGGCAGTG CTCGGTCTGG CTGCGTACTT CCGCAGCTTC GCGCCAATGT	240
TCACGCTCAG TACCGAACTC GGGGGGGGTG ATGCGCGCAGT GTCCGCTGAC ACTGGGCTGC	300
CGGTGCGGGT GGCTCTGCTG GCTGCGCTGC TTGCGGGGT GTTCTCTGTC CCTAAGGCCA	360
AGAGCCATGT GACGGTAGTT GCGGTGCTCG GGGTACTCGG CGTATTCTG ATGGTCTCGG	420
CGACCTTTAA CAAGCCGAGC GCTATTGCA CCGGTTGGGC ATTGTGGGT GTTTGGCTT	480
TCATCGTGT CCAGGCGGT GCGGCACTCC TGGCGCTCTT GGTGGAGACC GCGCTATCA	540
CGCGCGCGGC GCGCGCGGCC AAGTTCGACC CGTATGACA GTACGGCGCG TACCGGCACT	600
ACGCGCAGTA CCGGCTGCAG CCGGTGGGT ACTACGGTCA GCAGGCTGCT CAGCAGGCGG	660
CGGCACTGCA GTGCGCGCGC CCGCAGCACT CTCGCGAGCC TCGCGATAT GGTTCGCACT	720
ACGCGCGCTA TTGCTGCACT CCGAGCCAAT CCGGCACTGG ATACACTGCT CAGCGCGCGG	780
CGCAGCGCGC GCGCACTGC GGGTGCAGC AATCGCAGCA GCGCGCATTC ACCCGACCTA	840
CGCGCTTTCC GAGCTTCAGC CCACCACCAC CGTCACTGC CCGGACGGGG TCGCAGGCTG	900
GTTGCGCTCC AGTCAACTAT TCAAACCCCA GCGGGGGCGA GCAGTCTCTC TCGCCGCGG	960
GCGCGCGCGT CTAACCGCGC GTTCCGCGCT CCGGTGCGGC GTGTGCGCGA AGAGTGAACA	1020
GCGTGTGAGC AAGCGCGGAC GATCTCTGTC CGGAATTC	1058

(12) INFORMATION FOR SEQ ID NO:46:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA GACCGATGCC GTTACCTCTG CGCAGGAGGC AGGTAAATTC GACCGGATCT	60
CCGCGGACCT GAAACCCAG ATGACCCAGG TGGAGTCGAC GGCAGGTTCC TTCCAGGCCC	120

```

AGTGGCGCGG CGCGCGCGGG ACGGCCCGCC AGGCCCGCGT GGTGCGCTTC CAAGAAGCAG      180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTGCTCAG GCGGCGCTCC      240
AATACTCGAG GCTCGACGAG GAGCAGCAGC AGGCCCTGTC CTCGCAATG GGCTTCTGAC      300
CCGCTAATAC GAAAGAAAC GGAGCAA                                           327

```

## (2) INFORMATION FOR SEQ ID NO:47:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CGGTGCGCAT GATGGCGTTG TCGAACCTGA CGATTCTGT ACCGCGCTCG TTGAGATCAA      60
CCAACAACGT GTTGGCGTCC GCAAATGTGC CGACCCGCTG GATCTCGGTG ATCTTCTTCT      120
TCTTCATCAG GAAGTGACA CCGGCCACCC TCGCTCGGN TACCTTTCGG      170

```

## (2) INFORMATION FOR SEQ ID NO:48:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GATCGCGCGG CACGGGGGCT GCGGCCGCGA GCACCGCTGG CGCTCGCGGC AACCGCGGGG      60
CGCGGGGTGG CGCGGAACC GTTGGTTGC TCTTCGCGAA CGGCGGTGCC GCGGGGCAAG      120
GGGCGGT                                           127

```

## (2) INFORMATION FOR SEQ ID NO:49:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

CGGCGGCAAG GGCGGCACCG CCGCAAGCG GAGCGGCGCG GCGGCGCGCA ACGGCGCGCA      60
CGGCGGCTCG GCGTCAACG G                                           81

```

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCTGCTCC GGCAGAAAGC GCGTAACCG AGGAGCTGCC GGATTGTTTC	60
GCAACGGGCG GCGCGGNGGT GCGGGCGCGT CCAACCAAGC CGGTAACCGC GGNGCGGCGC	120
GAACCGGTGG TCGCGGTGGG CTGATCTGG	149

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACAGAA TCACACTTAC CAGTGATCG AGATCGTGG GACCTGGCCC GACGCTGTCC	60
ACCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGGCGAGAC CATCCGCGCG CTGACTGXT	120
TGGAATACA GTCAATTGAA GGCACCTGG TCGACGAGC GGTCCGCGAC TTCCAGGTGA	180
CTATGAAAGT CGCTTCCGC CTGAGGATT CCTGAACCTT CAAGCGCGGC CGATACTGA	240
GGTGATCAT TAAGGACTT TTCCAGACA TCTGACCG CTGAAACGC GGTTCAGCC	300
ACGTTGCTC CGCGAGGCG CTGCTCCAA AATCCCTCG ACAATTCCTC GGCG	355

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 999 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCAC ATCACCATCA CATGCATCAG GTGGACGCCA ACTTGACAGC TCACAAGGGA	60
CGATTGCGCG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG	120
CGCGGAGCG CCAACGCGCA TCGGAGCCA GCGCCCCCG TACCCACAAC GCGCGCTCG	180
CGCGCTCGA CGGCTGCAGC GCGACCGCA CCGCGAGAC CTGTTCCCGC CCGACACCG	240